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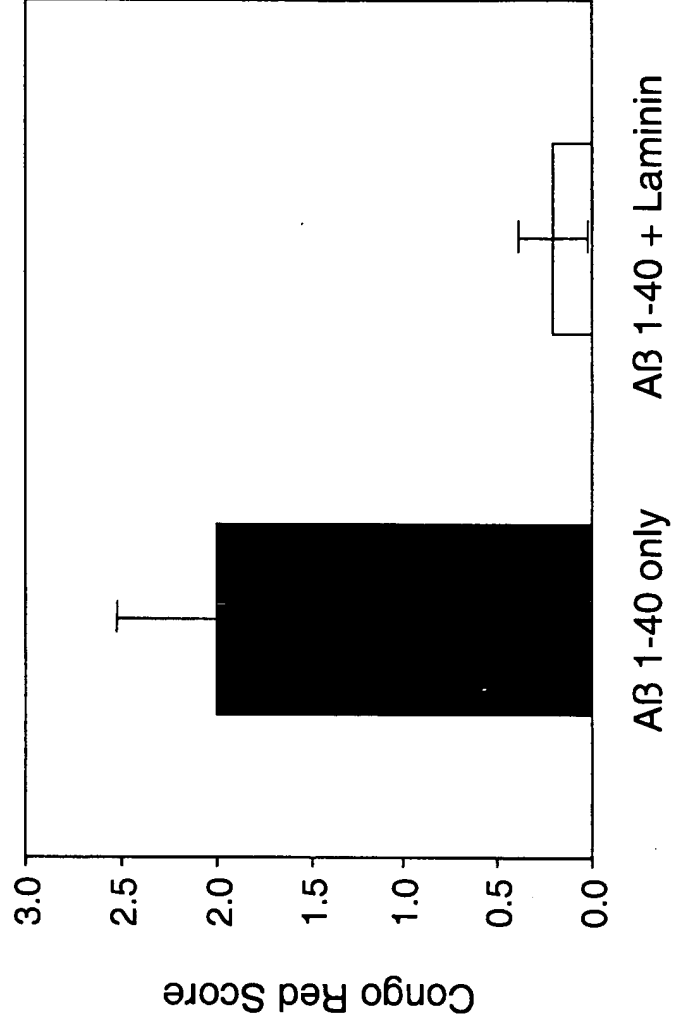


Figure 1

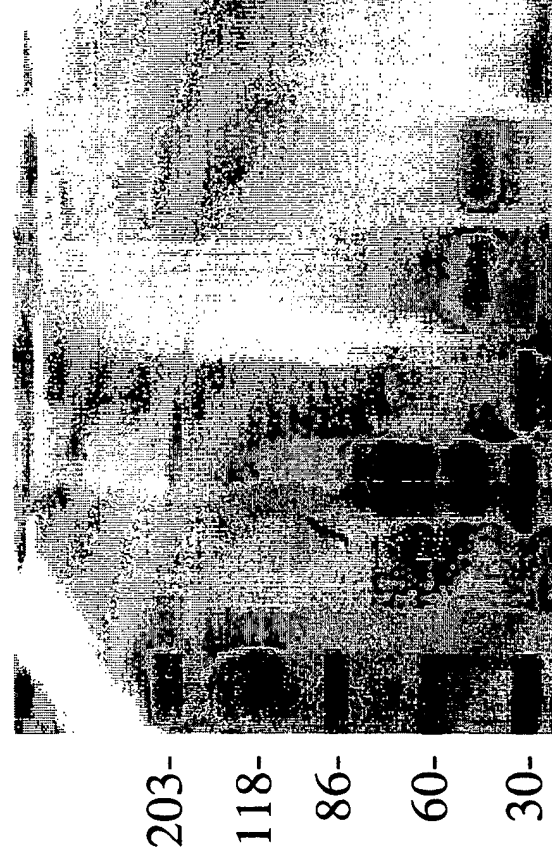


Figure 2

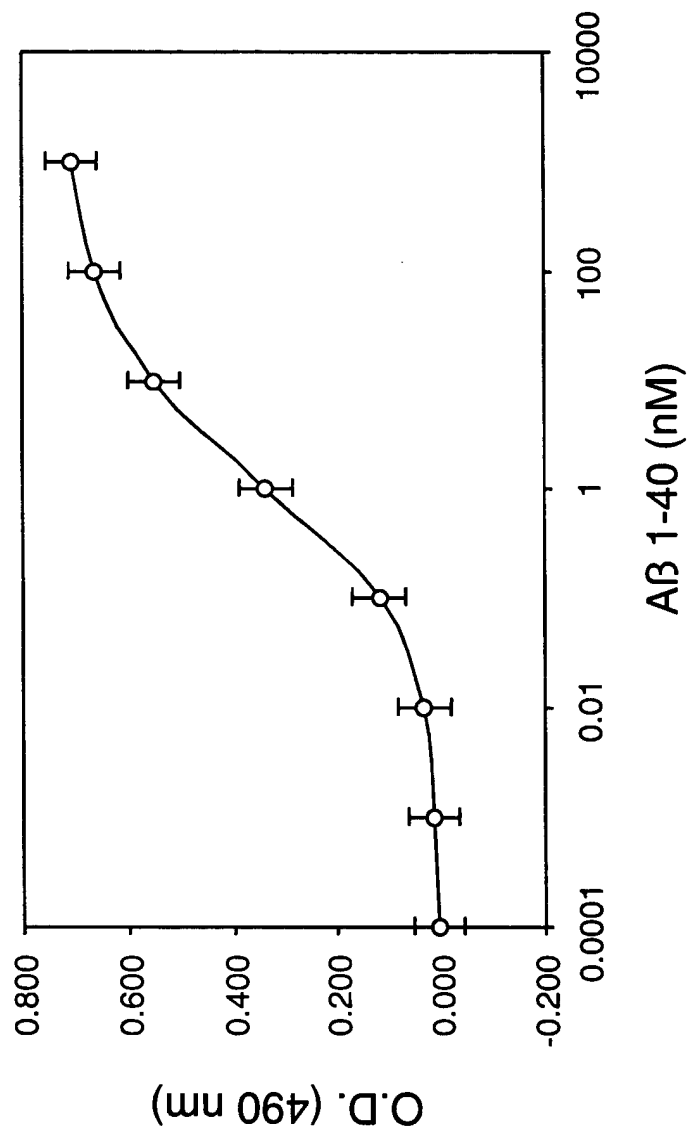


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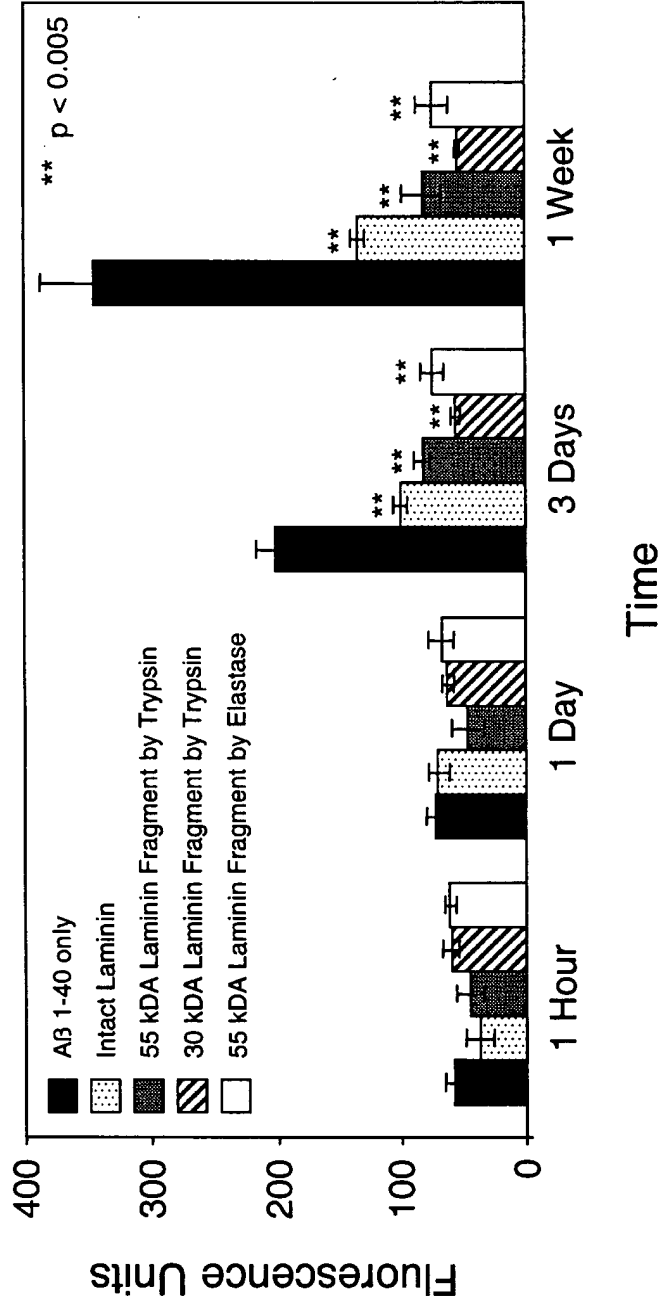


Figure 4

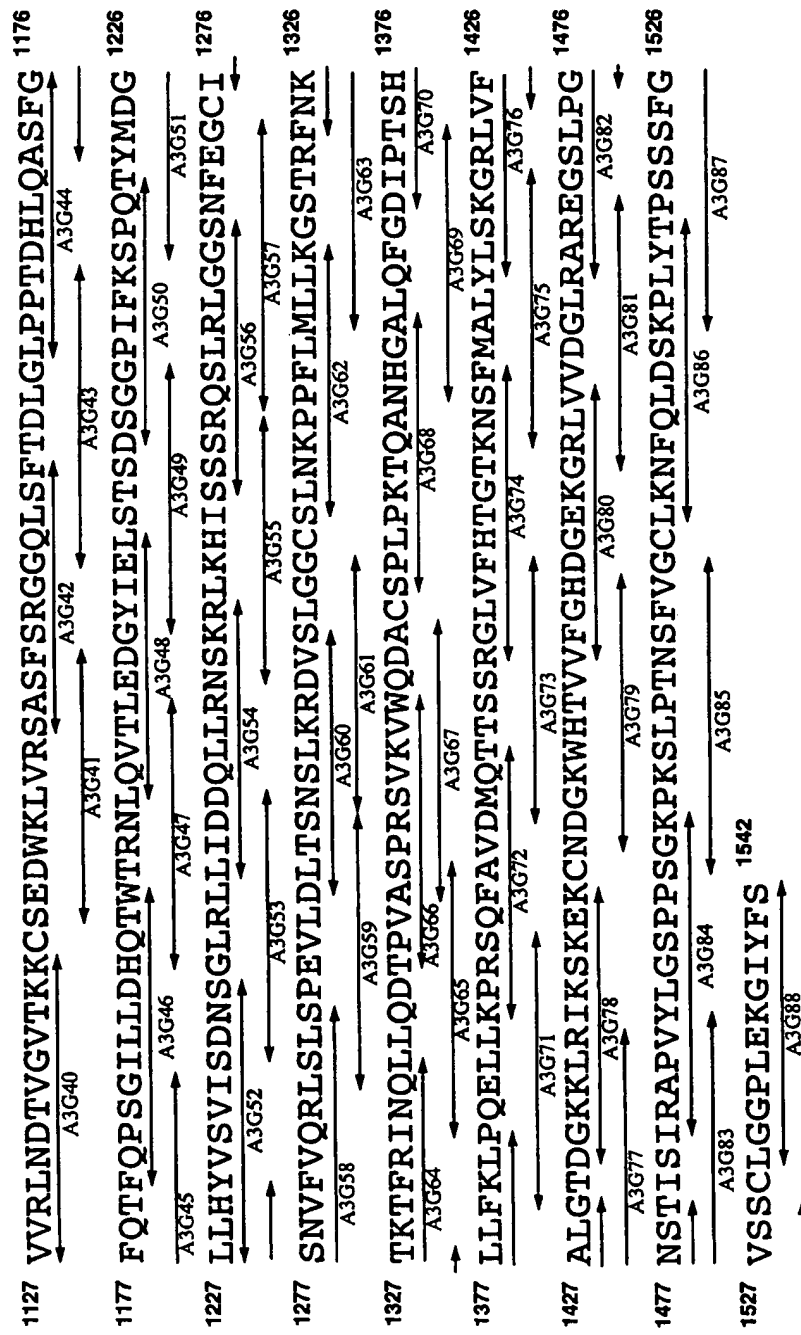


Figure 5

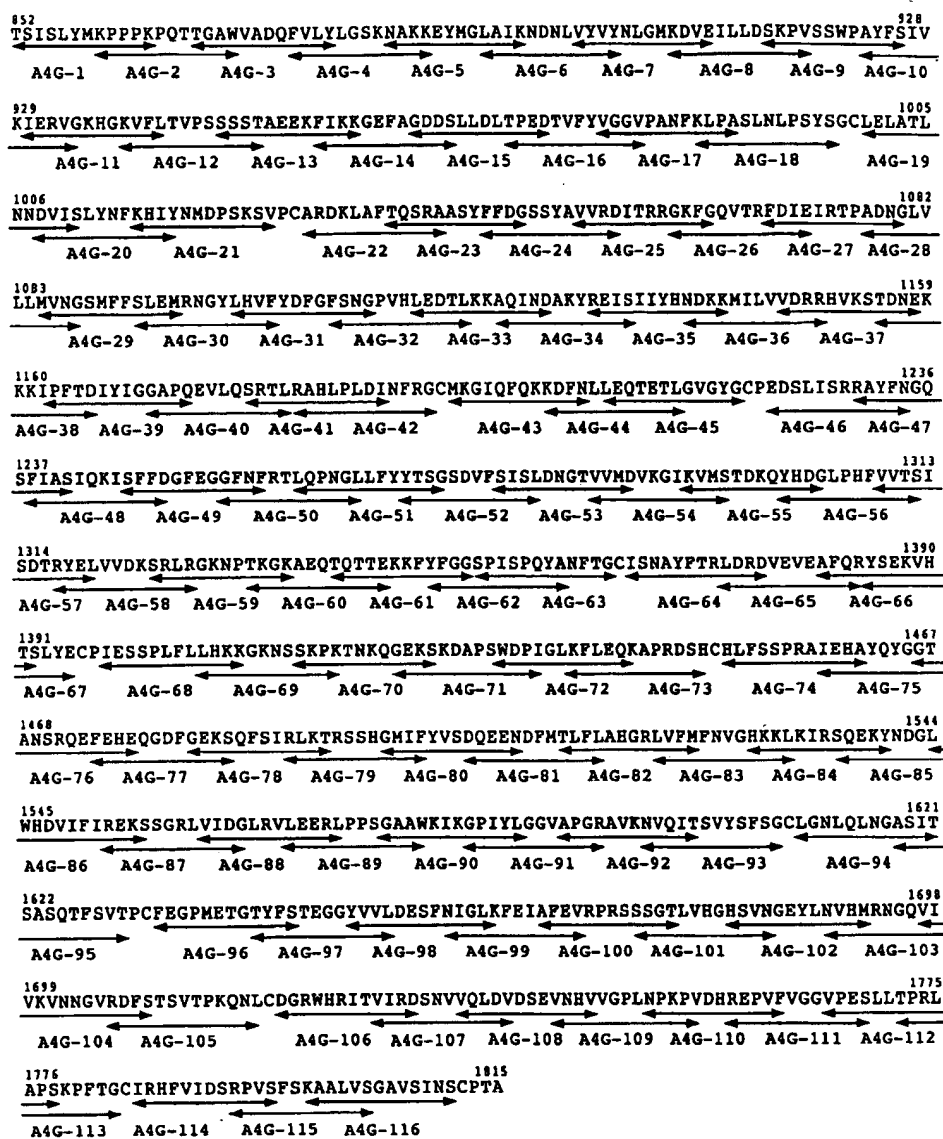


Figure 6

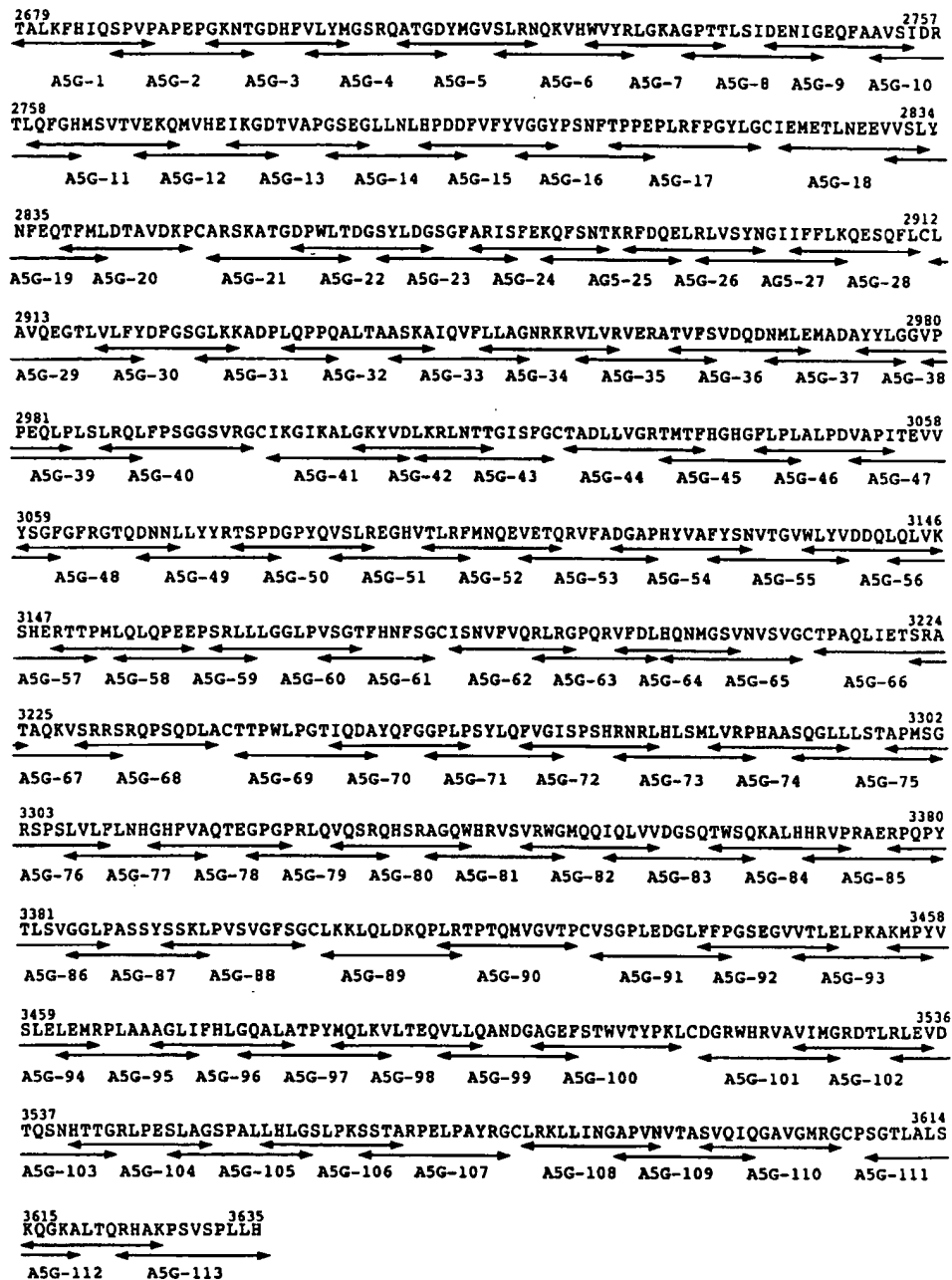


Figure 7

| PEPTIDES | Laminin Chain and Amino Acid Sequence Number | Amino Acid Sequence | % Disruption/ Disassembly of Fibrillar AB (AB:Peptide Molar Ratio of 1:6) |
|----------|--|---------------------|--|
| AG73 | Alpha-1 chain; residues 2719-2730 | RKRLQVQLSIRT | 46 % (S; p < 0.01)*** |
| A3 | Alpha-3 chain; residues 2243-2254 | KPRLQFSLDIQT | 23 % (S; p < 0.01) |
| A5 | Alpha-5 chain; residues 3275-3286 | RNRLHLSMLVRP | 22 % (S; p<0.01) |
| C-16 | Gamma-1 chain; residues 139-150 | KAFDITYVRLKF | 28 % (S; p<0.01)*** |
| LAM-L | Alpha-1 chain; residues 2097-2108 | AASIKVAVSADR | 24 % (S; p<0.01) |
| A-13 | Alpha-1 chain; residues 97-109 | RQVFQVAYIIKA | 30 % (S; p<0.01)*** |
| HA3G45 | Alpha-3 chain; residues 1173-1184 | ASFQFQTFQPSG | 21 % (S; p<0.05) |
| HA3G47 | Alpha-3 chain; residues 1189-2000 | HQTWTRNLQVTL | 28 % (S; p<0.01)*** |
| HA3G58 | Alpha-3 chain; residues 1276-1287 | ISNVFVQRLSLS | 32 % (S; p<0.01)*** |
| HA3G67 | Alpha-3 chain; residues 1342-1353 | ASPPSVKVVQDA | 25 % (S; p<0.01)*** |
| HA3G71 | Alpha-3 chain; residues 1379-1390 | FKLPQELLKPRS | 23 % (S; p<0.05) |
| HA3G74 | Alpha-3 chain; residues 1402-1414 | RGLVFHTGTKNSF | 32 % (S; p<0.01)*** |
| HA3G75 | Alpha-3 chain; residues 1411-1422 | KNSFMALYLSKG | 24 % (S; p<0.01) |
| HA3G76 | Alpha-3 chain; residues 1418-1429 | YLSKGRLVFALG | 26 % (S; p<0.01)*** |
| HA3G79 | Alpha-3 chain; residues 1444-1455 | NDGKWHTVVFGH | 27 % (S; p<0.01)*** |
| HA3G83 | Alpha-3 chain; residues 1477-1487 | GNSTISIRAPVY | 33 % (S; p<0.01)*** |
| A4G31 | Alpha-4 chain; residues 1101-1112 | LHVFYDFGFSNG | 23 % (S; p<0.01) |
| A4G82 | Alpha-4 chain; residues 1513-1524 | TLFLAHGRLVFM | 30 % (S; p<0.01)*** |
| A5G15 | Alpha-5 chain; residues 2792-2803 | HPDDFVFYVGGY | 30 % (S; p<0.01)*** |
| A5G35 | Alpha-5 chain; residues 2950-2961 | VLVRVERATVFS | 20 % (S; p<0.05) |
| A5G46 | Alpha-5 chain; residues 3043-3054 | FLPLALPDVAPI | 21 % (S; p<0.05) |
| A5G56 | Alpha-5 chain; residues 3135-3146 | WLYVDDQLQLVK | 27 % (S; p<0.01)*** |
| A5G71 | Alpha-5 chain; residues 3259-3270 | GPLPSYLQFVGI | 22 % (S; p<0.05) |
| A5G80 | Alpha-5 chain; residues 3329-3340 | VQSRQHSRAGQW | 25 % (S; p<0.01)*** |
| A5G81 | Alpha-5 chain; residues 3337-3348 | AGQWHRVSVRWG | 41 % (S; p<0.01)*** |
| A5G82 | Alpha-5 chain; residues 3345-3356 | VRWGMQQIQLVV | 29 % (S; p<0.01)*** |
| A5G84 | Alpha-5 chain; residues 3361-3372 | TWSQKALHHRVP | 27 % (S; p<0.01)*** |
| A5G101 | Alpha-5 chain; residues 3516-3527 | DGRWHRVAVIMG | 39 % (S; p<0.01)*** |
| A5G109 | Alpha-5 chain; residues 3587-3598 | APVNV TASVQIQ | 32 % (S; p<0.01)*** |
| A5G110 | Alpha-5 chain; residues 3594-3605 | SVQIQGAVGMRG | 23 % (S; p<0.05) |

*** Selected for Further Testing

Figure 8

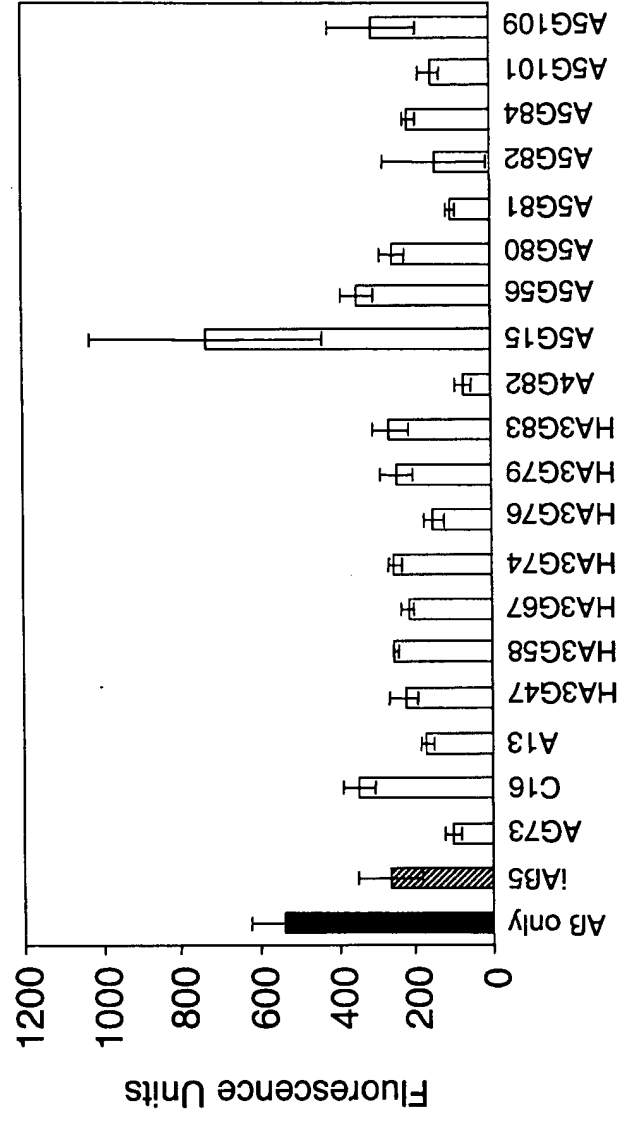


Figure 9

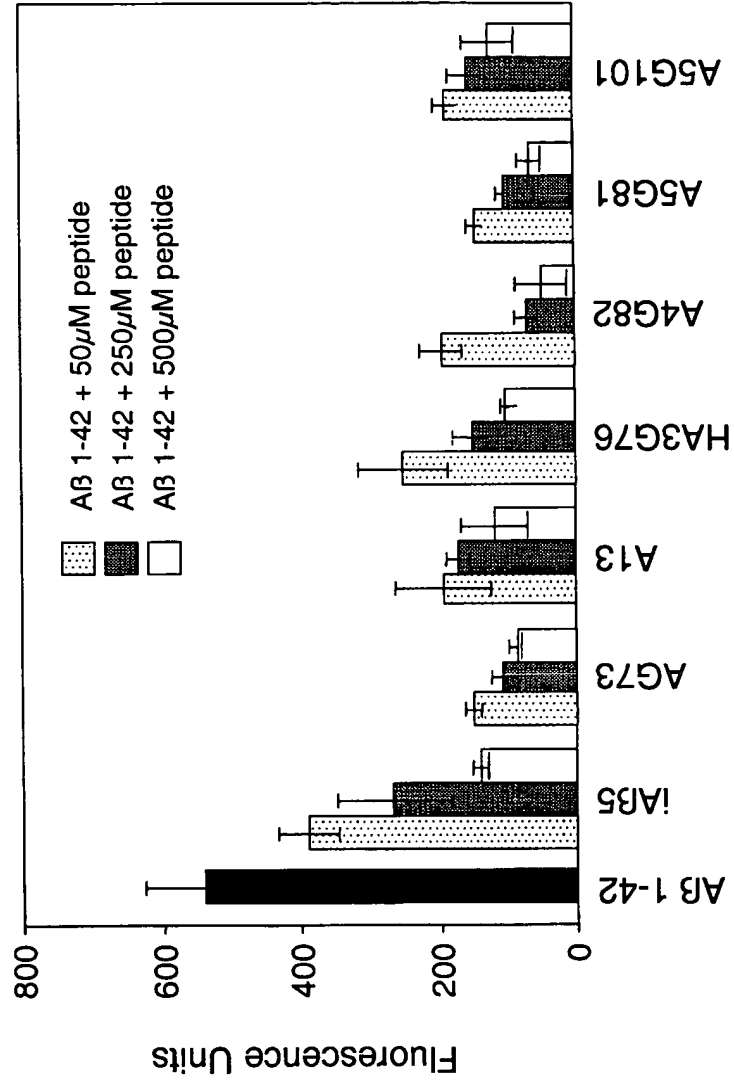


Figure 10

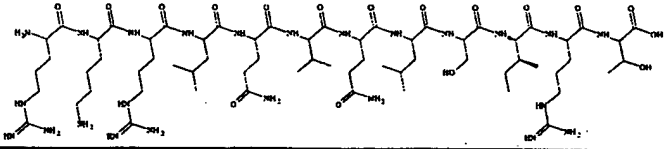
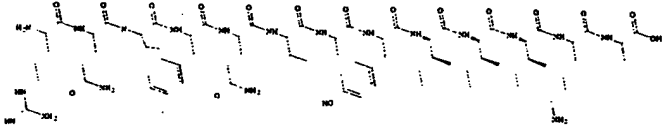
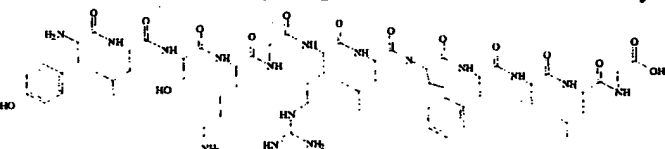
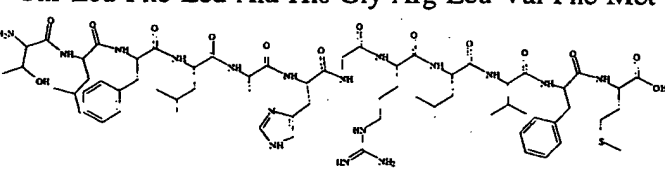
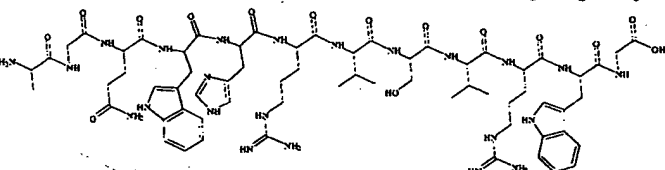
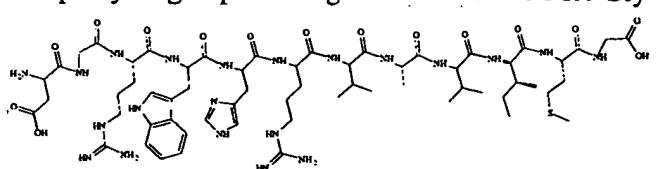
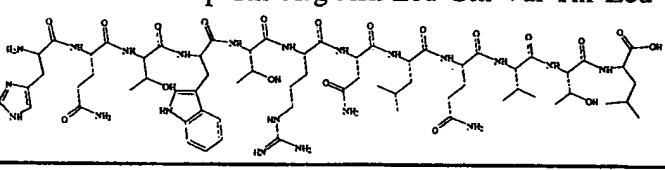
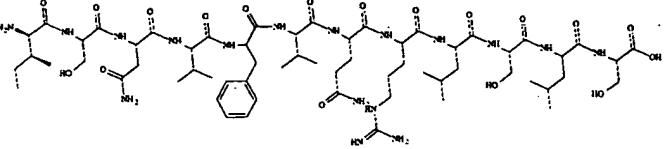
| PTI- | Structure | Formula | MW |
|---|--|------------------------------|---------|
| DP-001 D-AG73 or D-A1 A1-chain 2719-2730 | Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr  | $C_{64}H_{120}N_{24}O_{17}$ | 1497.82 |
| DP-002 D-A13 A1-chain 97-109 | Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Lys-Ala  | $C_{74}H_{121}N_{19}O_{17}$ | 1548.90 |
| DP-003 D-HA3G76 A3-chain 1418-1429 | Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly  | $C_{63}H_{102}N_{16}O_{15}$ | 1323.61 |
| DP-004 D-A4G82 A4-chain 1513-1524 | Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met  | $C_{67}H_{105}N_{17}O_{14}S$ | 1404.75 |
| DP-005 D-A5G81 A5-chain 3337-3348 | Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly  | $C_{65}H_{95}N_{23}O_{15}$ | 1438.62 |
| DP-006 D-A5G101 A5-chain 3516-3527 | Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly  | $C_{61}H_{97}N_{21}O_{15}S$ | 1396.65 |
| DP-007 D-HA3G47 A3-chain 1189-2000 | His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu  | $C_{66}H_{105}N_{21}O_{19}$ | 1496.70 |
| DP-008 D-HA3G58 A3-chain 1276-1287 | Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser  | $C_{61}H_{103}N_{17}O_{18}$ | 1362.60 |

Fig. 12a

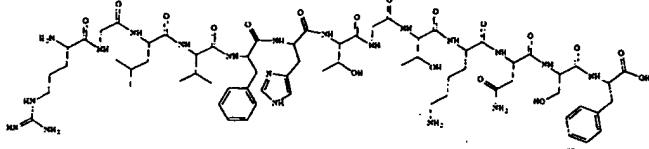
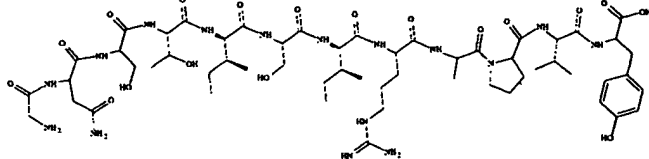
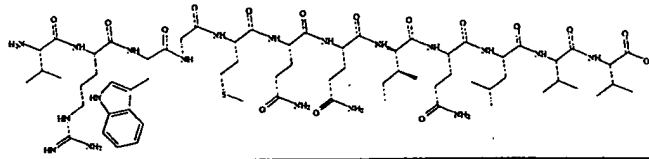
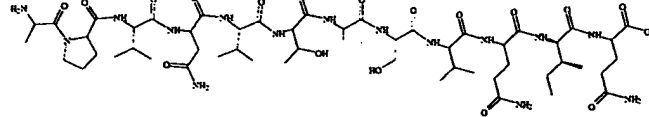
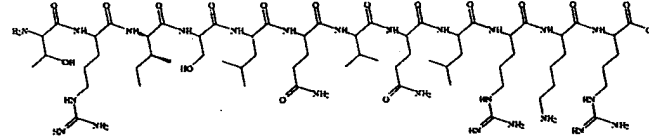
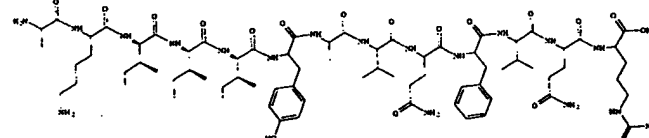
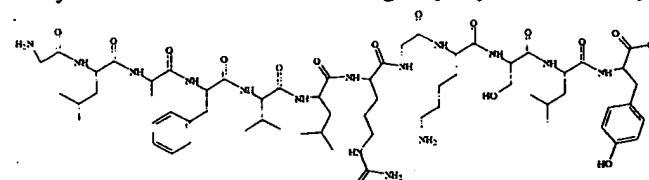
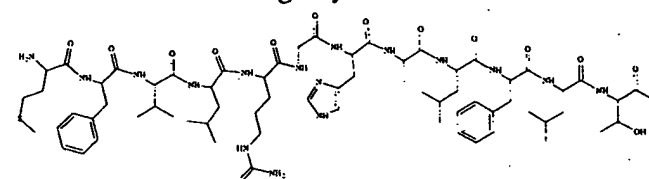
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| DP-009 D-HA3G74 A3-chain 1402-1414 | Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe  | $C_{66}H_{102}N_{20}O_{18}$ | 1463.67 |
| DP-010 D-HA3G83 A3-chain 1477-1487 | Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr  | $C_{56}H_{92}N_{16}O_{18}$ | 1277.45 |
| DP-011 D-A5G82 A5-chain 3345-3356 | Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val  | $C_{66}H_{109}N_{19}O_{16}S$ | 1456.78 |
| DP-012 D-A5G109 A3-chain 1444-1455 | Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln  | $C_{53}H_{91}N_{15}O_{18}$ | 1226.40 |
| DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719 | Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg  | $C_{64}H_{120}N_{24}O_{17}$ | 1497.82 |
| DP-014 D-rA13 A1-chain r92-109 or 109-92 | Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg  | $C_{74}H_{121}N_{19}O_{17}$ | 1547.92 |
| DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418 | Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr  | $C_{63}H_{102}N_{16}O_{15}$ | 1323.61 |
| DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513 | Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr  | $C_{67}H_{105}N_{17}O_{14}S$ | 1404.75 |

Fig. 12b

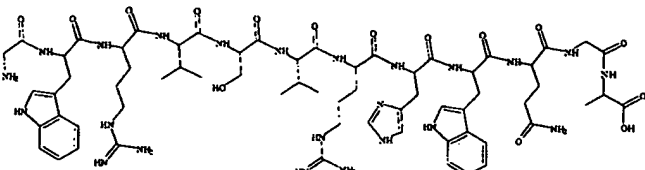
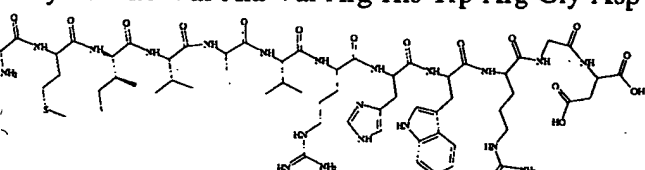
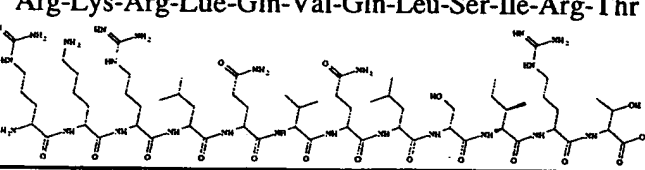
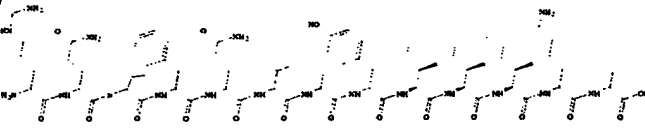
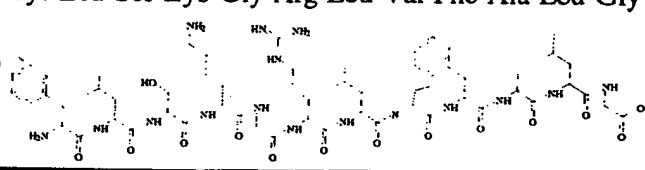
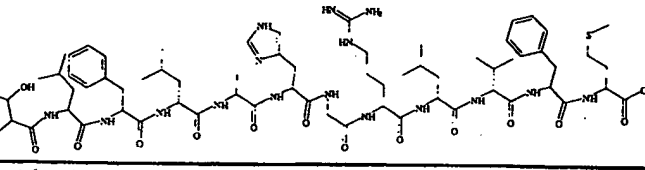
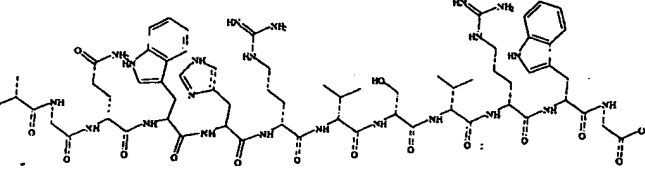
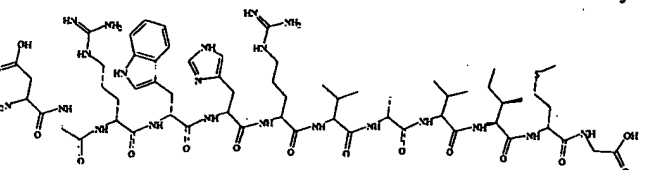
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| DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337 | Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala  | $C_{65}H_{95}N_{23}O_{15}$ | 1438.62 |
| DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516 | Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp  | $C_{61}H_{97}N_{21}O_{15}S$ | 1396.65 |
| LP-019 AG73 or A1 A1-chain 2719-2730 | Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr  | $C_{64}H_{120}N_{24}O_{17}$ | 1497.82 |
| LP-020 A13 A1-chain 92-109 | Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala  | $C_{74}H_{121}N_{19}O_{17}$ | 1548.90 |
| LP-021 HA3G76 A3-chain 1418-1429 | Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly  | $C_{63}H_{102}N_{16}O_{15}$ | 1323.61 |
| LP-022 A4G82 A4-chain 1513-1524 | Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly  | $C_{67}H_{105}N_{17}O_{14}S$ | 1404.75 |
| LP-023 A5G81 A5-chain 3337-3348 | Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly  | $C_{65}H_{95}N_{23}O_{15}$ | 1438.62 |
| LP-024 A5G101 A5-chain 3516-3527 | Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly  | $C_{61}H_{97}N_{21}O_{15}S$ | 1396.65 |

Fig. 12c

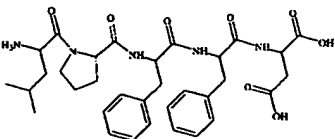
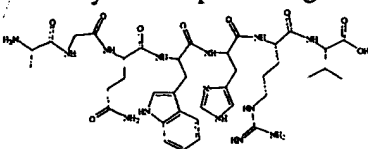
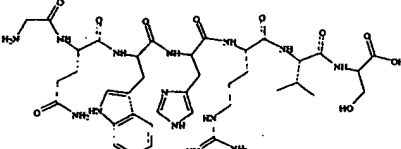
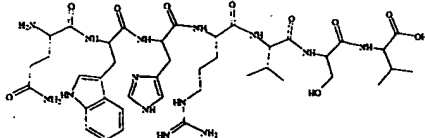
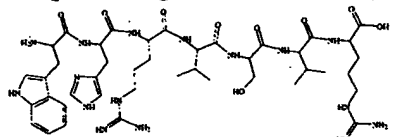
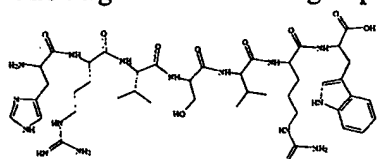
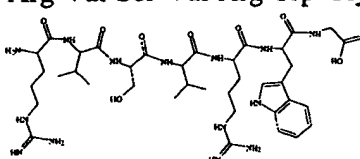
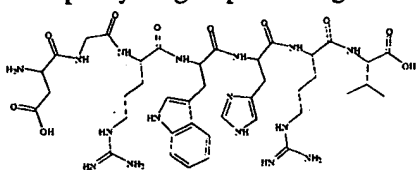
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| LP-025 β-sheet breaker or iAβ5 | Leu-Pro-Phe-Phe-Asp  | $C_{33}H_{43}N_5O_8$ | 637.74 |
| DP-026 Trc'n 5;1-7 | Ala-Gly-Gln-Trp-His-Arg-Val  | $C_{38}H_{56}N_{14}O_9$ | 852.95 |
| DP-027 Trc'n 5;2-8 | Gly-Gln-Trp-His-Arg-Val-Ser  | $C_{38}H_{56}N_{14}O_{10}$ | 868.95 |
| DP-028 Trc'n 5;3-9 | Gln-Trp-His-Arg-Val-Ser-Val  | $C_{41}H_{62}N_{14}O_{10}$ | 911.04 |
| DP-029 Trc'n 5;4-10 | Trp-His-Arg-Val-Ser-Val-Arg  | $C_{42}H_{66}N_{16}O_9$ | 939.09 |
| DP-030 Trc'n 5;5-11 | His-Arg-Val-Ser-Val-Arg-Trp  | $C_{42}H_{66}N_{16}O_9$ | 939.09 |
| DP-031 Trc'n 5;6-12 | Arg-Val-Ser-Val-Arg-Trp-Gly  | $C_{38}H_{62}N_{14}O_9$ | 859.00 |
| DP-032 Trc'n 6;1-7 | Asp-Gly-Arg-Trp-His-Arg-Val  | $C_{40}H_{60}N_{16}O_{10}$ | 925.02 |

Fig. 12d

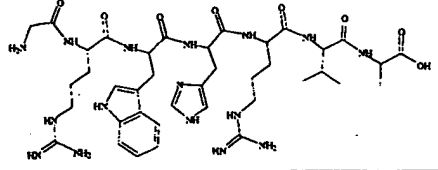
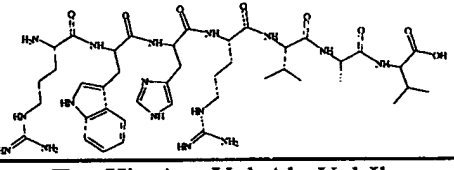
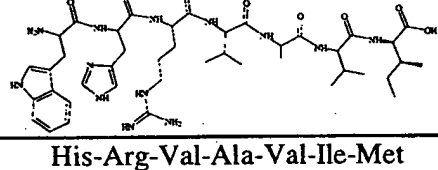
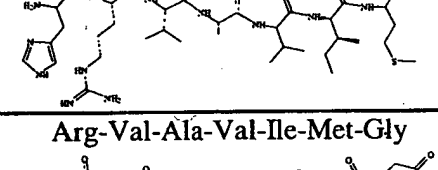
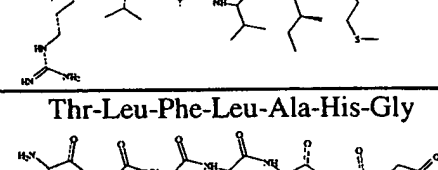
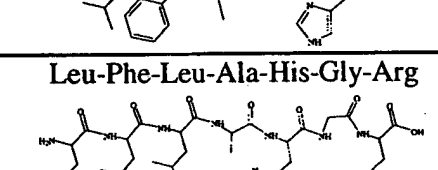
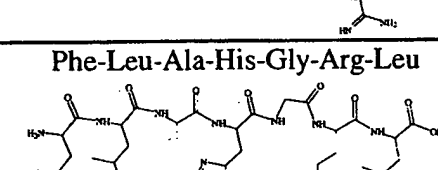
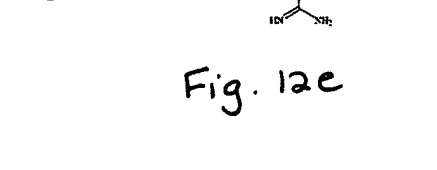
| PTI- | Structure | Formula | MW |
|---------------------------|--|--------------------------|--------|
| DP-033 Trc'n 6;2-8 | <p>Gly-Arg-Trp-His-Arg-Val-Ala</p>  | $C_{39}H_{60}N_{16}O_8$ | 881.01 |
| DP-034 Trc'n 6;3-9 | <p>Arg-Trp-His-Arg-Val-Ala-Val</p>  | $C_{42}H_{66}N_{16}O_8$ | 923.09 |
| DP-035 Trc'n 6;4-10 | <p>Trp-His-Arg-Val-Ala-Val-Ile</p>  | $C_{42}H_{65}N_{13}O_8$ | 880.07 |
| DP-036 Trc'n 6;5-11 | <p>His-Arg-Val-Ala-Val-Ile-Met</p>  | $C_{36}H_{64}N_{12}O_8S$ | 825.05 |
| DP-037 Trc'n 6;6-12 | <p>Arg-Val-Ala-Val-Ile-Met-Gly</p>  | $C_{32}H_{60}N_{10}O_8S$ | 744.96 |
| DP-038 Trc'n 4;1-7 | <p>Thr-Leu-Phe-Leu-Ala-His-Gly</p>  | $C_{36}H_{55}N_9O_9$ | 757.89 |
| DP-039 Trc'n 4;2-8 | <p>Leu-Phe-Leu-Ala-His-Gly-Arg</p>  | $C_{38}H_{60}N_{12}O_8$ | 812.97 |
| DP-040 Trc'n 4;3-9 | <p>Phe-Leu-Ala-His-Gly-Arg-Leu</p>  | $C_{38}H_{60}N_{12}O_8$ | 812.98 |

Fig. 12c

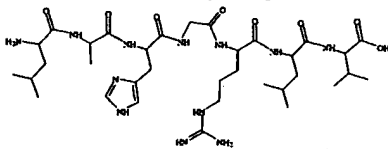
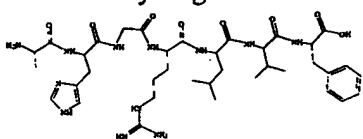
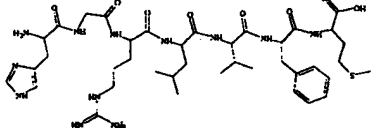
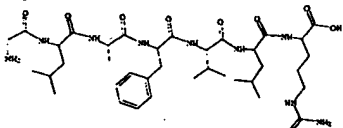
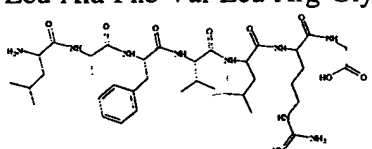
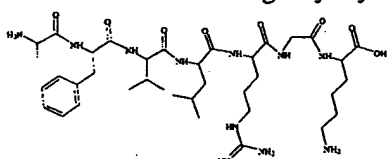
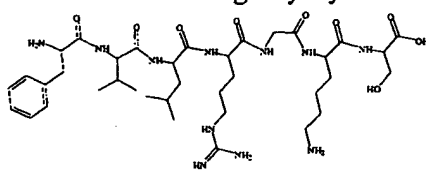
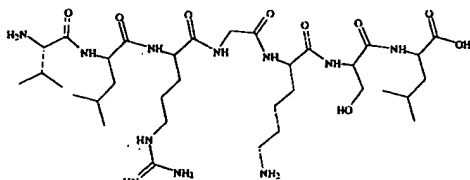
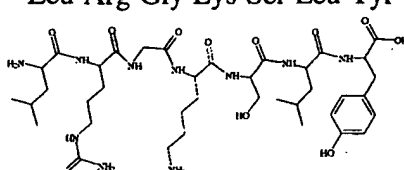
| PTI- | Structure | Formula | MW |
|----------------------------|---|----------------------------|--------|
| DP-041 Trc'n 4;4-10 | Leu-Ala-His-Gly-Arg-Leu-Val  | $C_{34}H_{60}N_{12}O_8$ | 764.93 |
| DP-042 Trc'n 4;5-11 | Ala-His-Gly-Arg-Leu-Val-Phe  | $C_{37}H_{58}N_{12}O_8$ | 798.95 |
| DP-043 Trc'n 4;6-12 | His-Gly-Arg-Leu-Val-Phe-Met  | $C_{39}H_{62}N_{12}O_8S$ | 859.07 |
| DP-044 Trc'n 15;1-7 | Gly-Leu-Ala-Phe-Val-Leu-Arg  | $C_{37}H_{62}N_{10}O_8$ | 774.97 |
| DP-045 Trc'n 15;2-8 | Leu-Ala-Phe-Val-Leu-Arg-Gly  | $C_{37}H_{62}N_{10}O_8$ | 774.97 |
| DP-046 Trc'n 15;3-9 | Ala-Phe-Val-Leu-Arg-Gly-Lys  | $C_{37}H_{63}N_{11}O_8$ | 789.98 |
| DP-047 Trc'n 15;4-10 | Phe-Val-Leu-Arg-Gly-Lys-Ser  | $C_{37}H_{63}N_{11}O_9$ | 805.98 |
| DP-048 Trc'n 15;5-11 | Val-Leu-Arg-Gly-Lys-Ser-Leu  | $C_{34}H_{65}N_{11}O_9$ | 771.96 |
| DP-049 Trc'n 15;6-2 | Leu-Arg-Gly-Lys-Ser-Leu-Tyr  | $C_{38}H_{65}N_{11}O_{10}$ | 836.01 |

Fig. 12f

In Vitro Screening of Laminin Peptides

ThioT

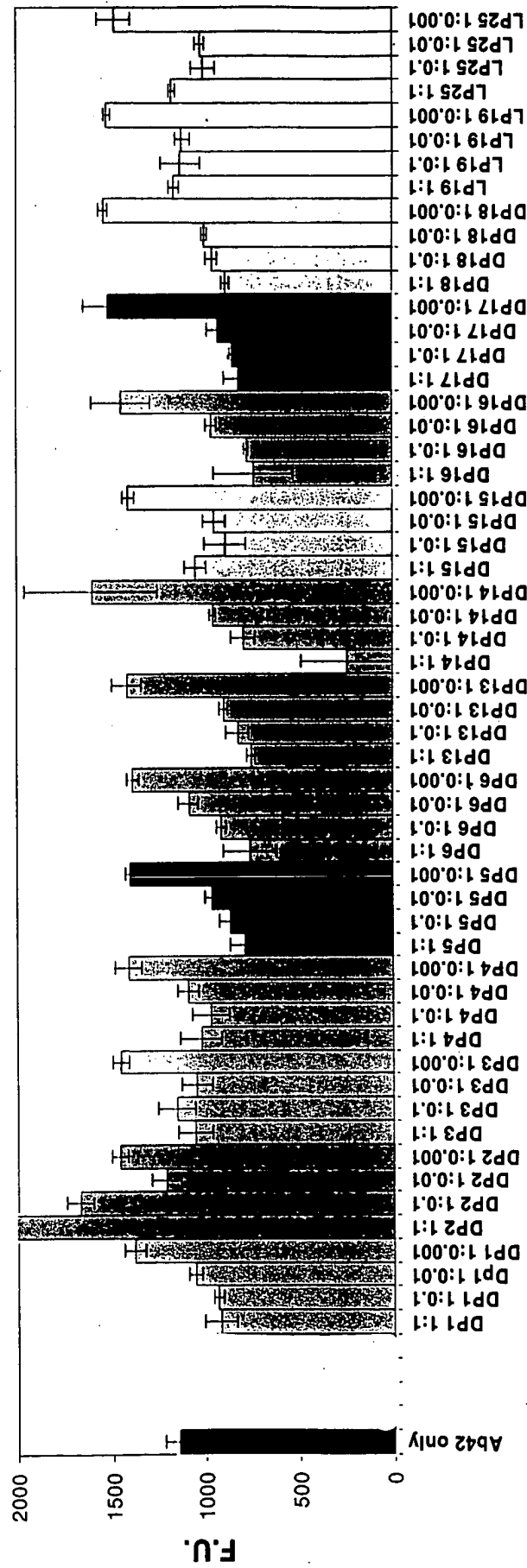


Fig. 13

In Vitro Screening of Laminin Peptides

Congo Red Binding of Ab42 +/- Laminin Peptides

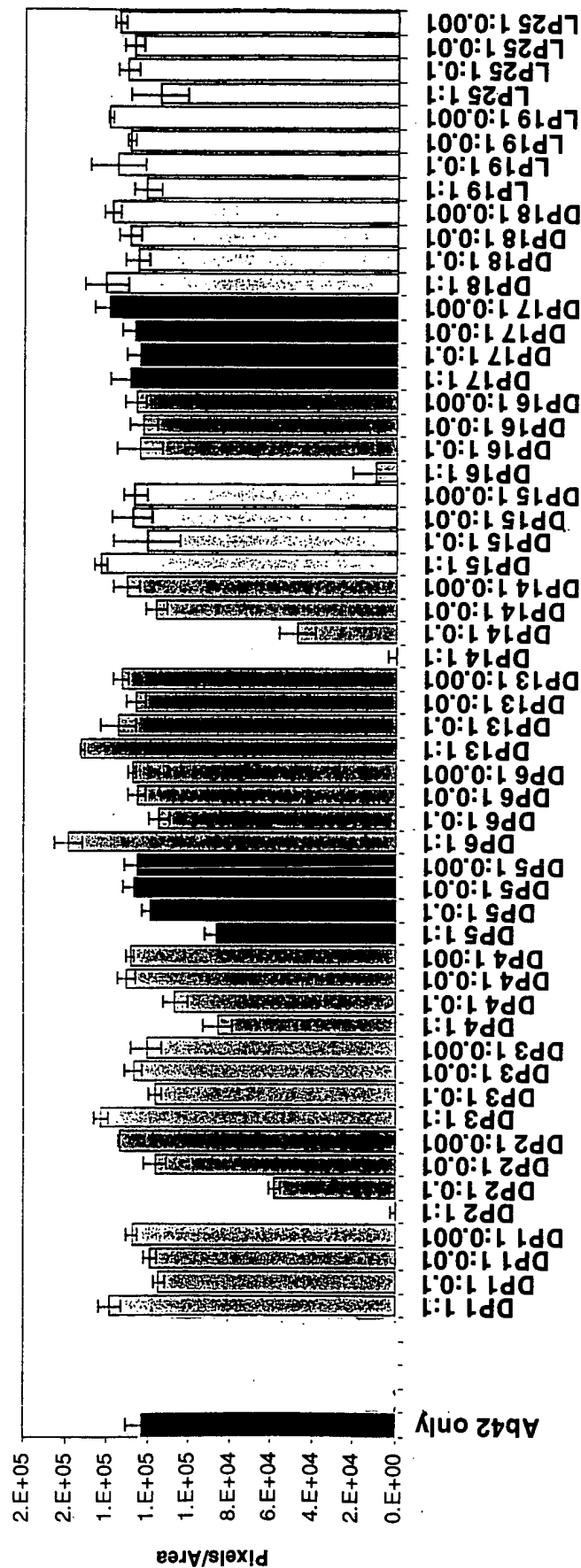


Fig. 14

In Vitro Screening of Laminin Peptides

ThioT

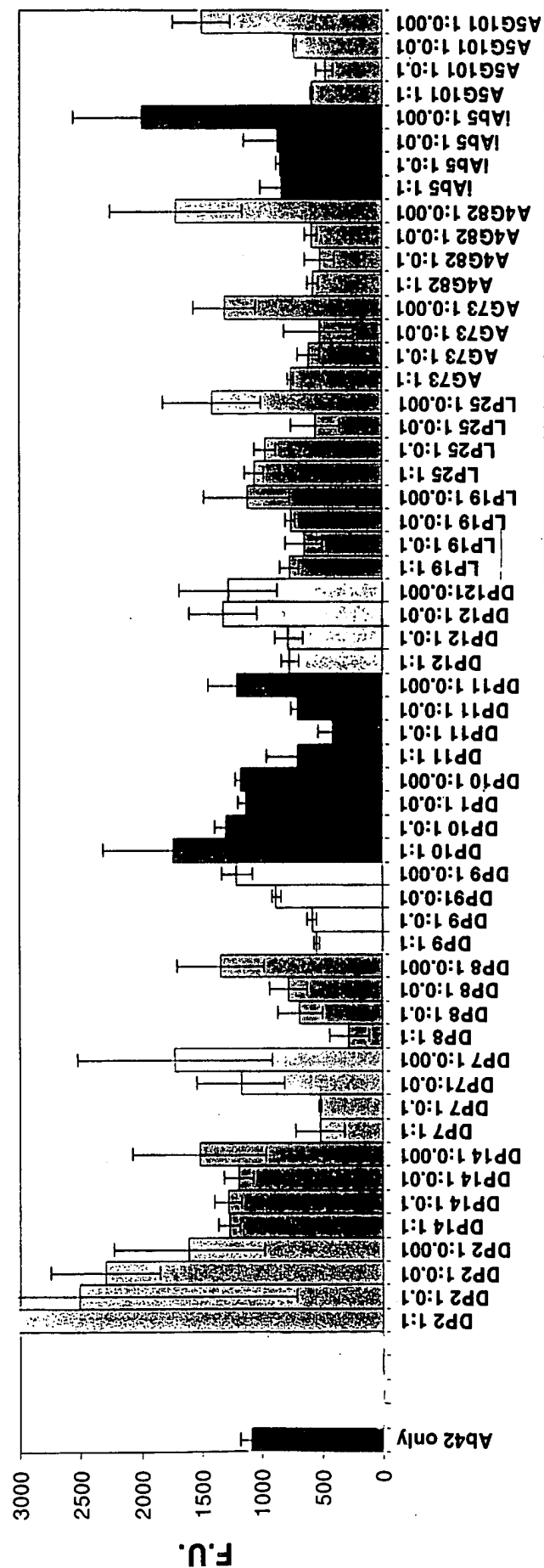
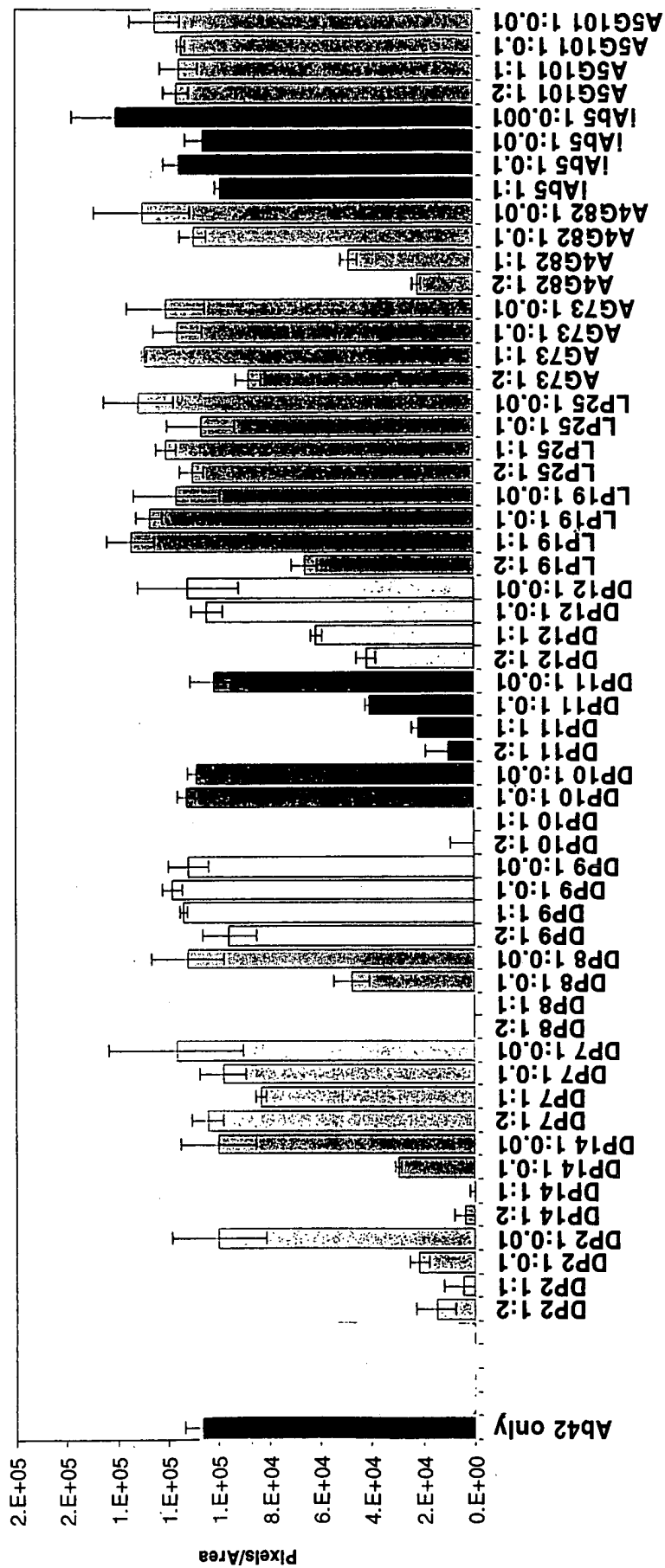
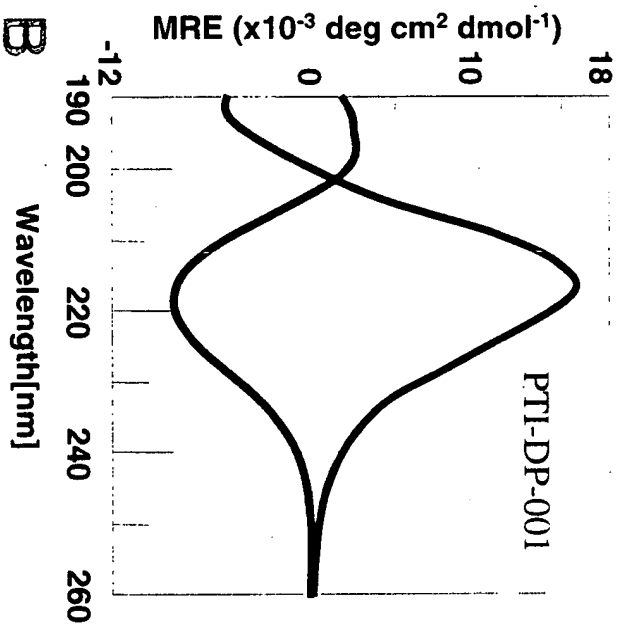
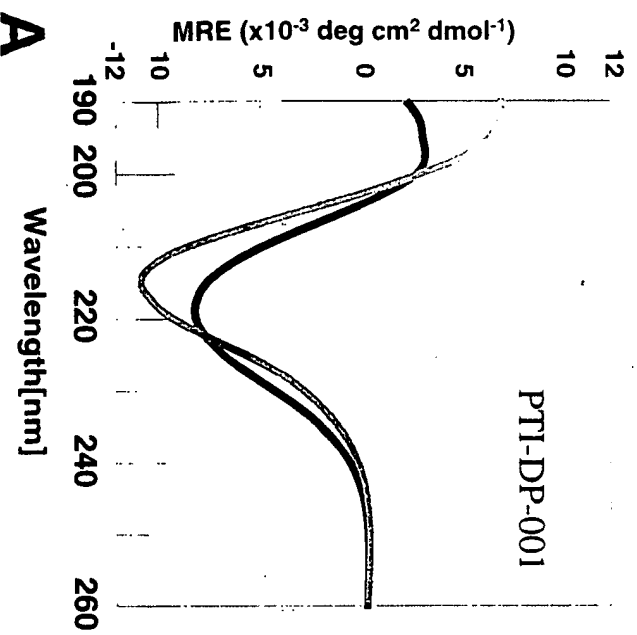


Fig. 15

In Vitro Screening of Laminin Peptides

Congo Red Binding of A β 42





Legend:

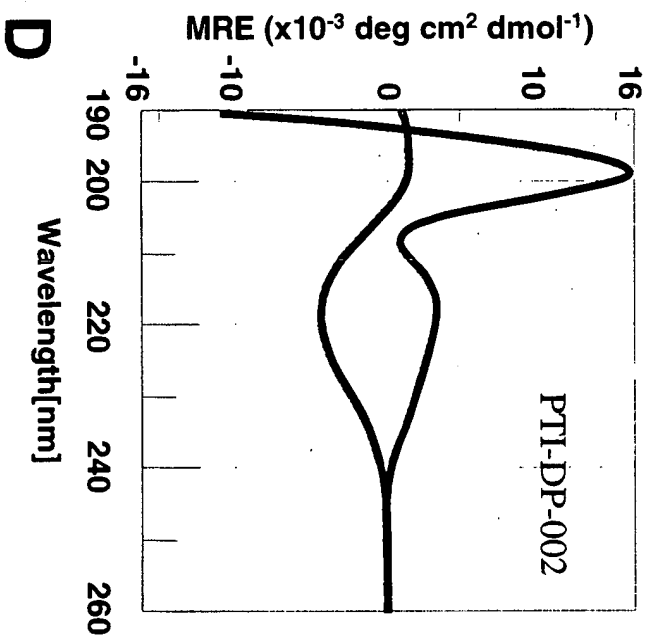
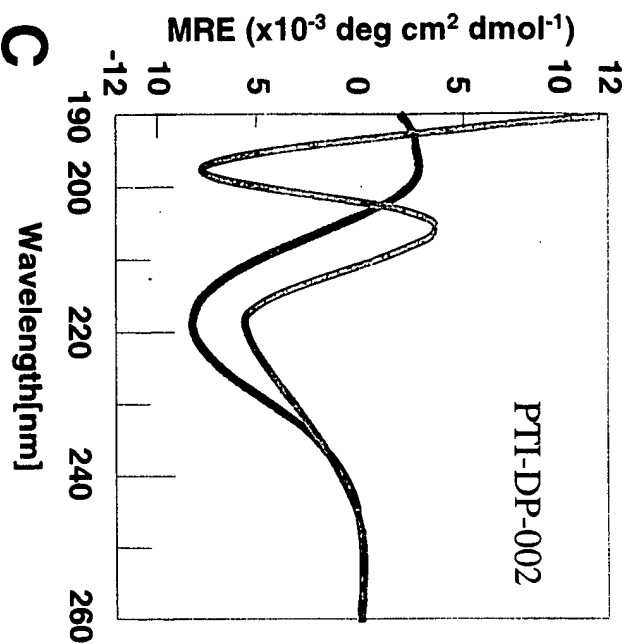
AB42 Only —

0.1 mg/ml —

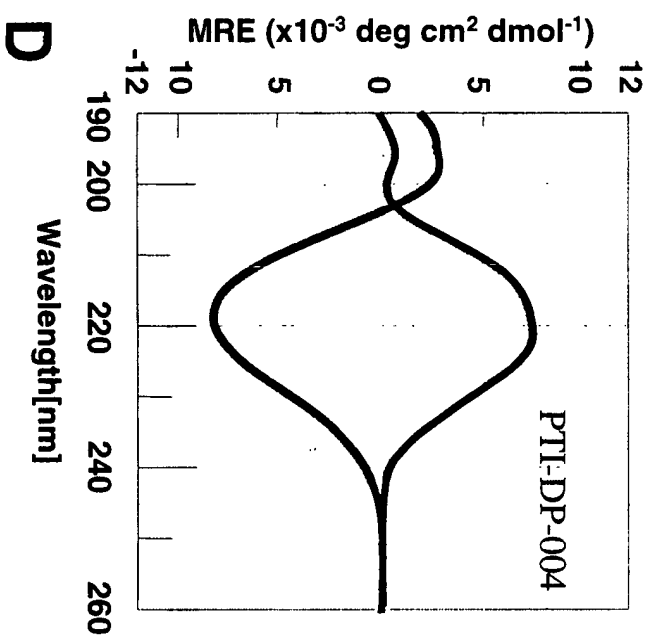
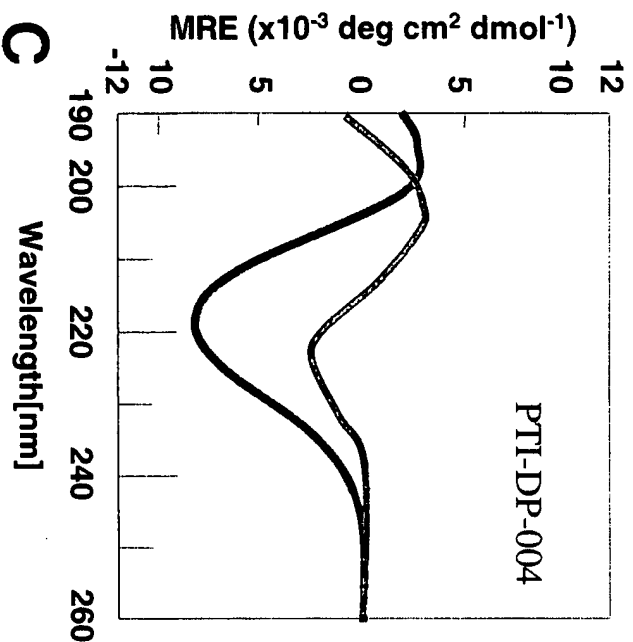
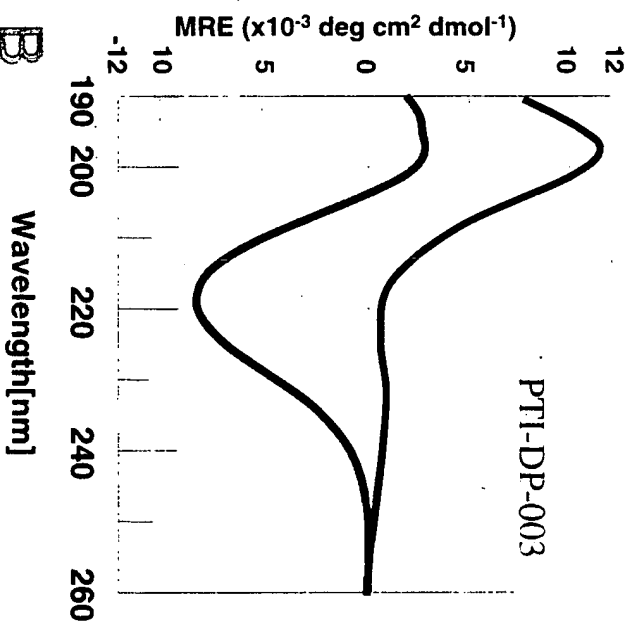
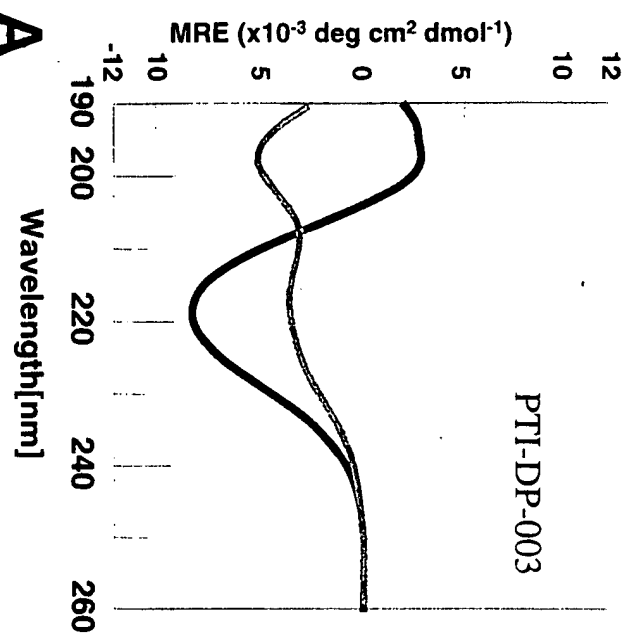
PTI-compound only —

0.2 mg/ml —

AB42 + PTI-compound 1:2 w/wt —



CD#34



Legend:

Aβ42 Only —

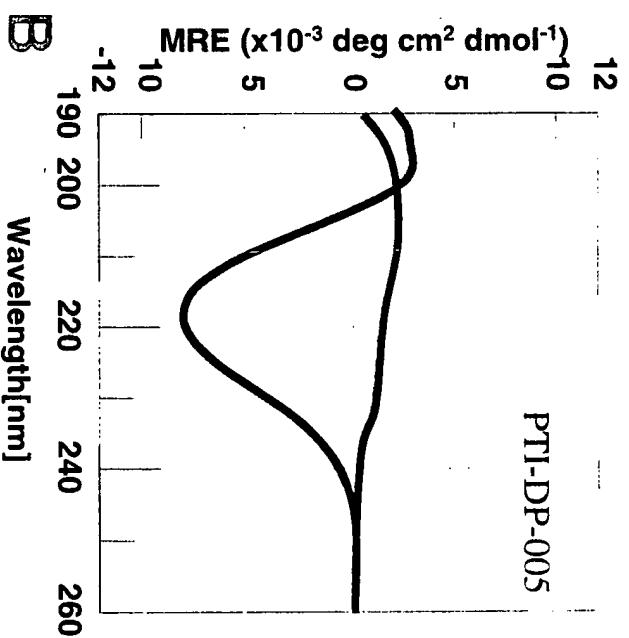
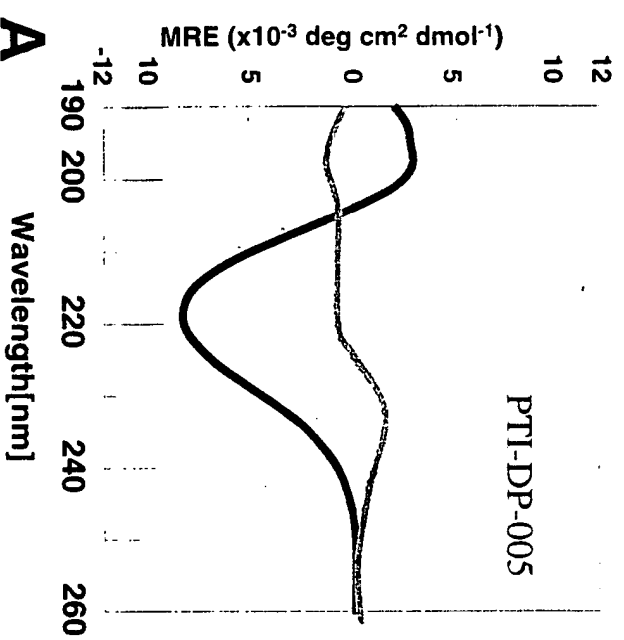
0.1 mg/ml

PTI-compound only —

0.2 mg/ml

Aβ42 + PTI-compound —

1:2 w/wt



Legend:

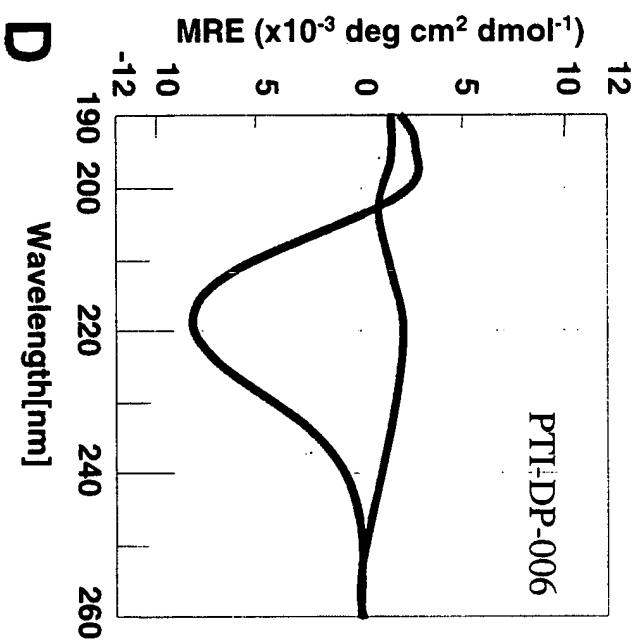
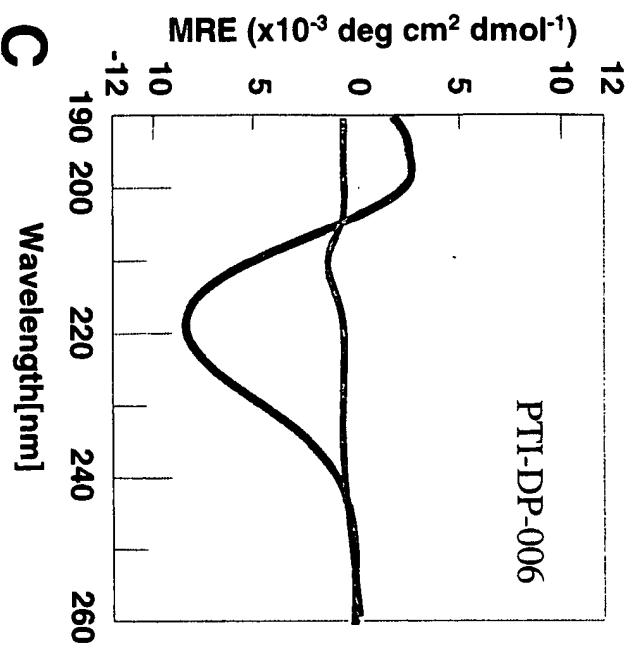
AB42 Only —

0.1 mg/ml —

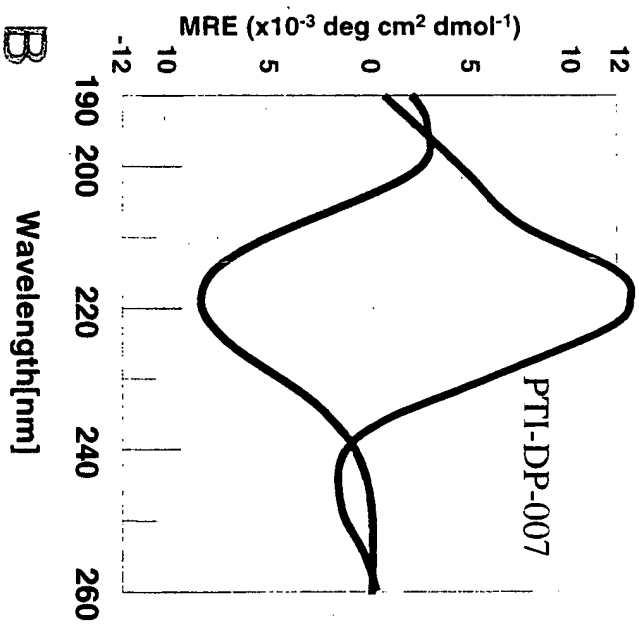
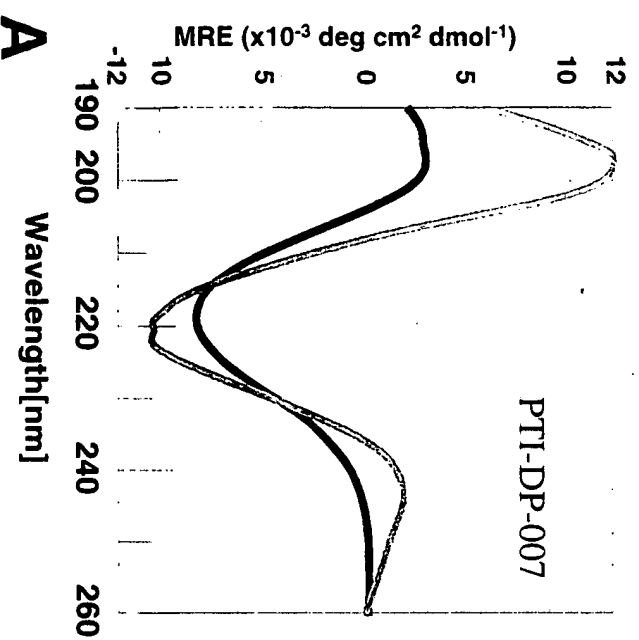
PTI-compound only —

0.2 mg/ml —

AB42 + PTI-compound 1:2 wt/wt —



CD#33

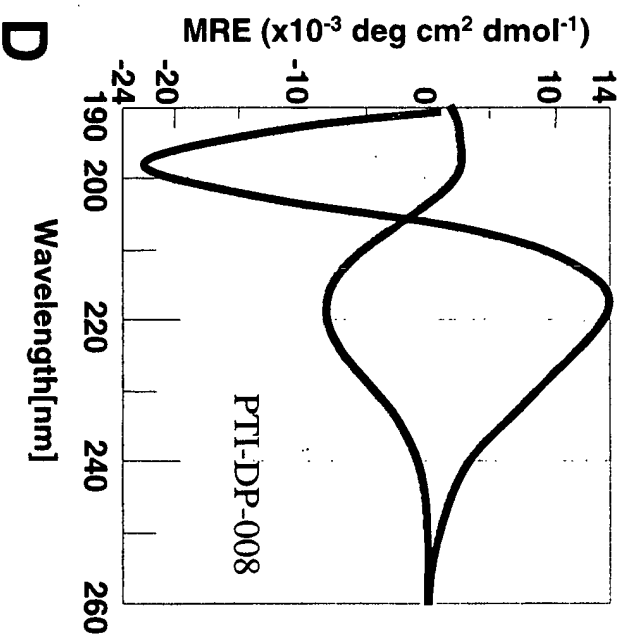
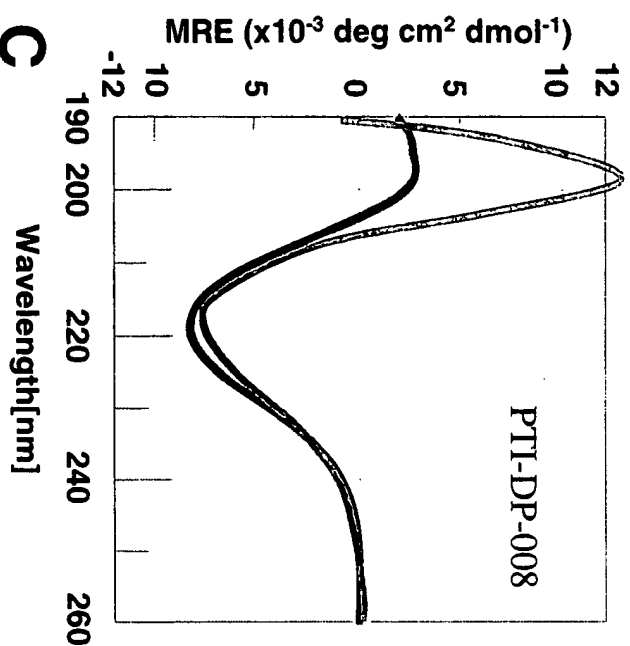


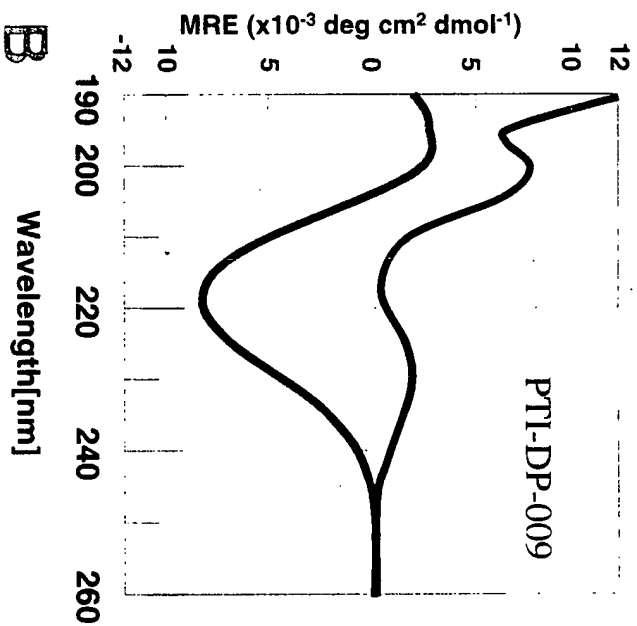
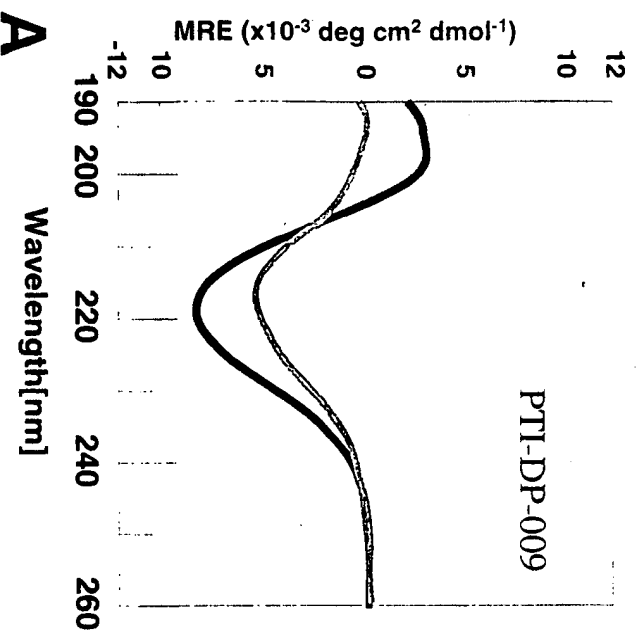
Legend:

AB42 Only —

PTI-compound only —

AB42 + PTI-compound 1:2 w/wt —





Legend:

AB42 Only —

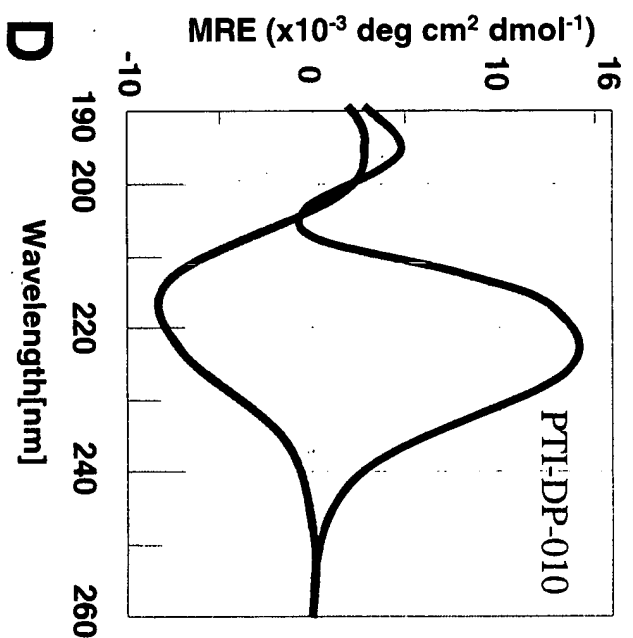
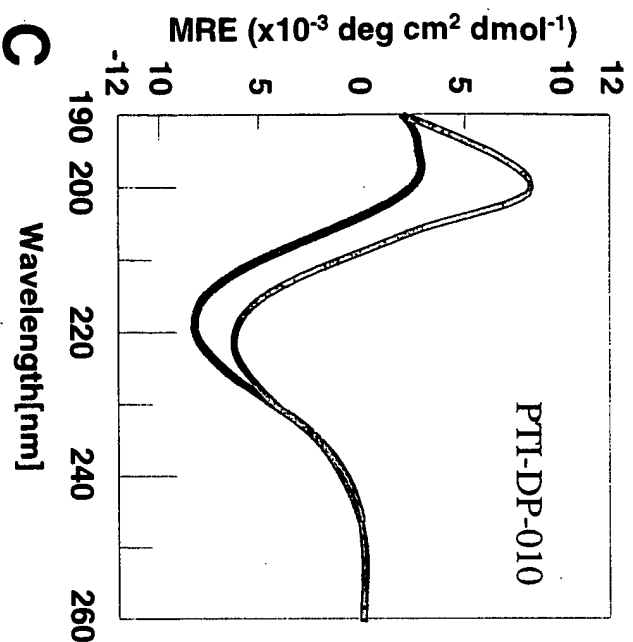
0.1 mg/ml —

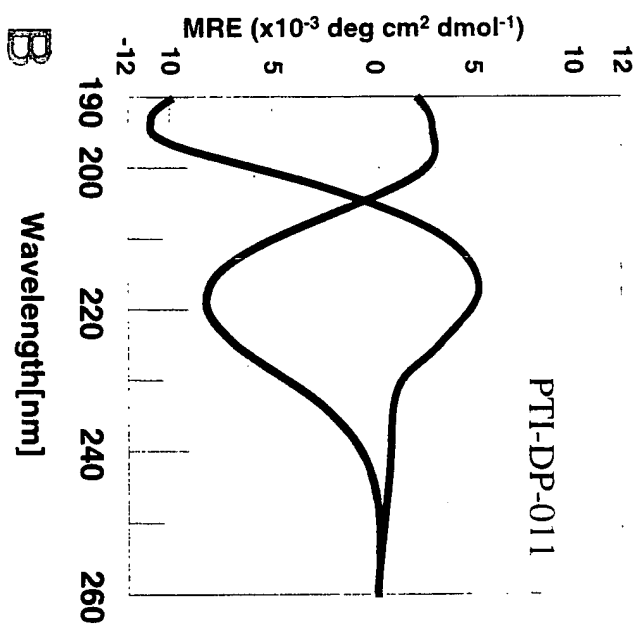
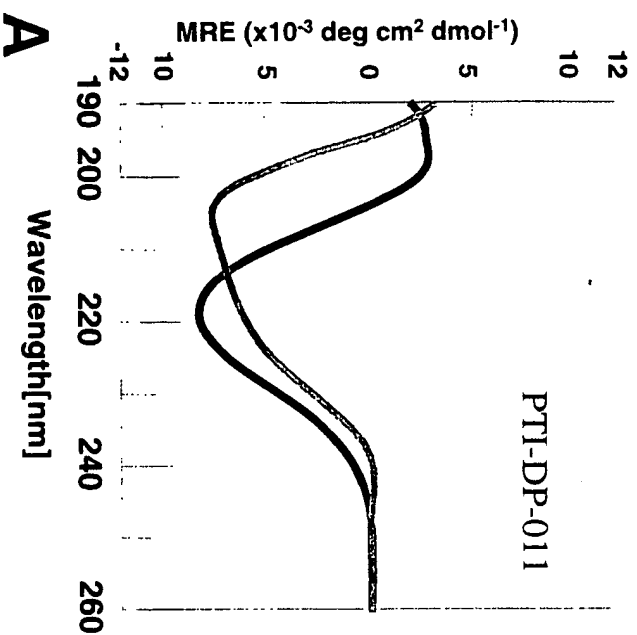
PTI-compound only —

0.2 mg/ml —

AB42 + PTI-compound 1:2 w/wt —

Fig. 21





Legend:

Aβ42 Only —

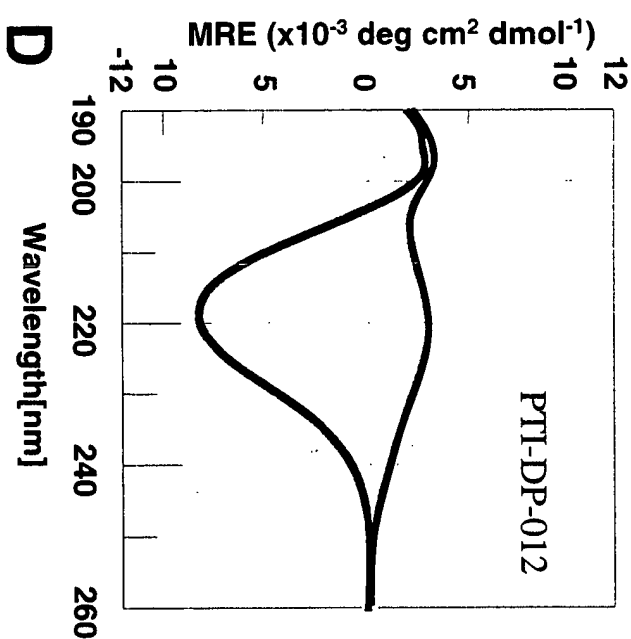
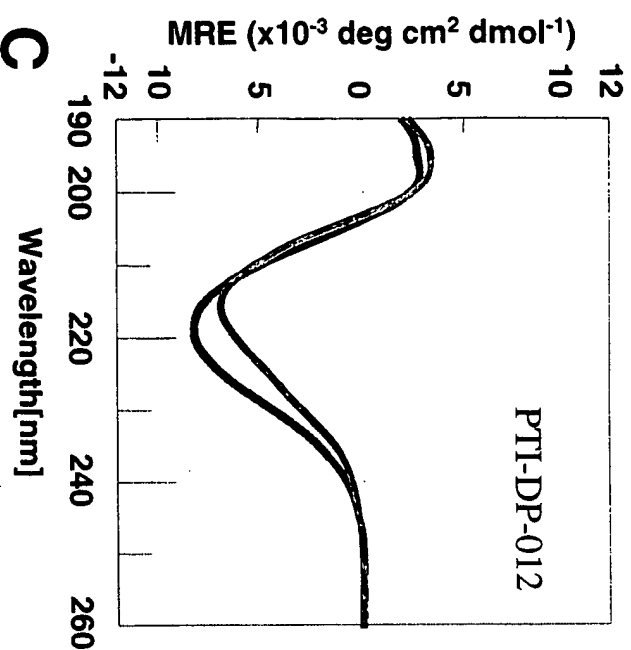
0.1 mg/ml —

PTI-compound only —

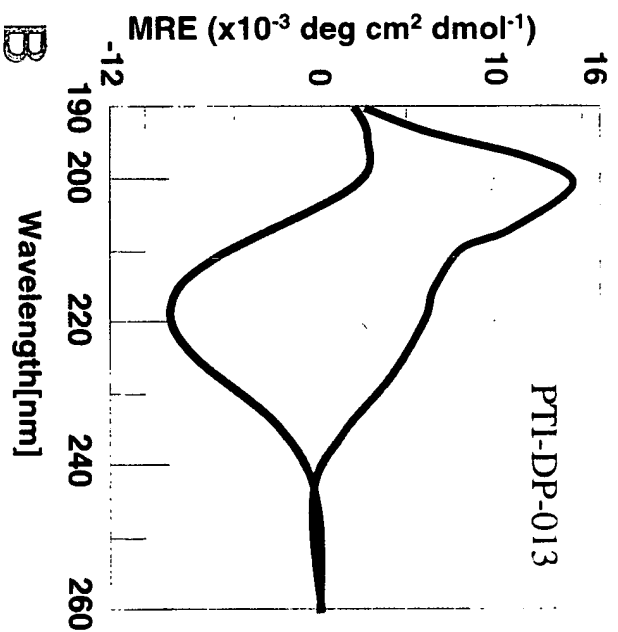
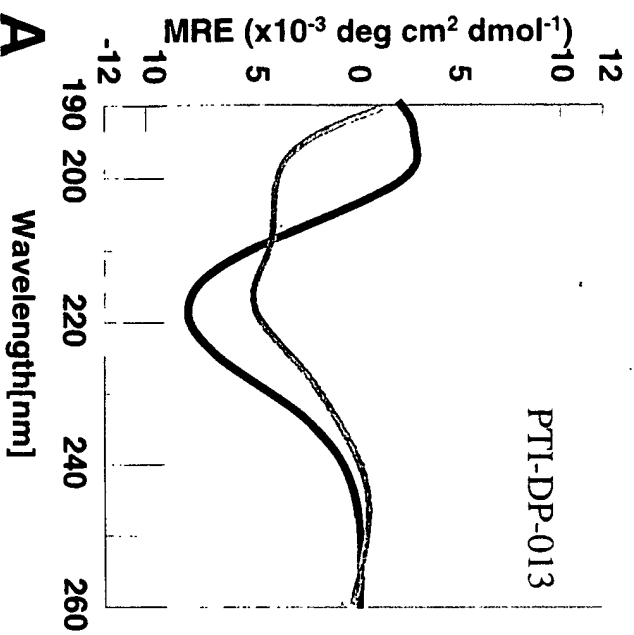
0.2 mg/ml —

Aβ42 + PTI-compound 1:2 w/w1 —

Fig. 22



CD#34



Legend:

Aβ42 Only —

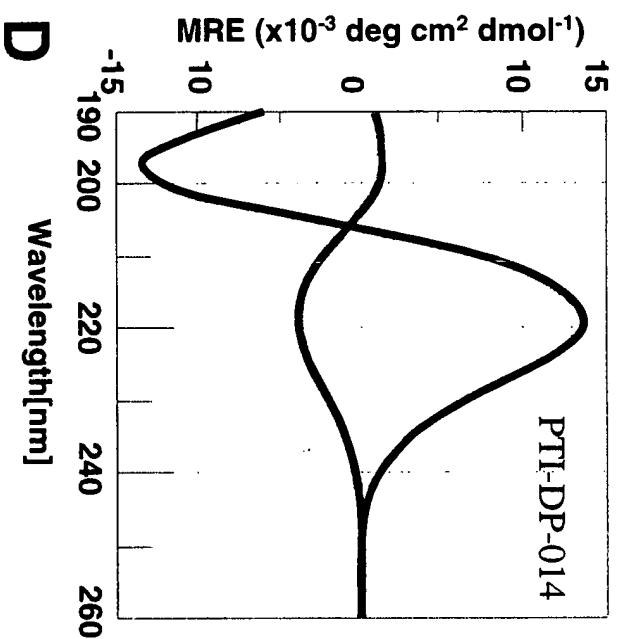
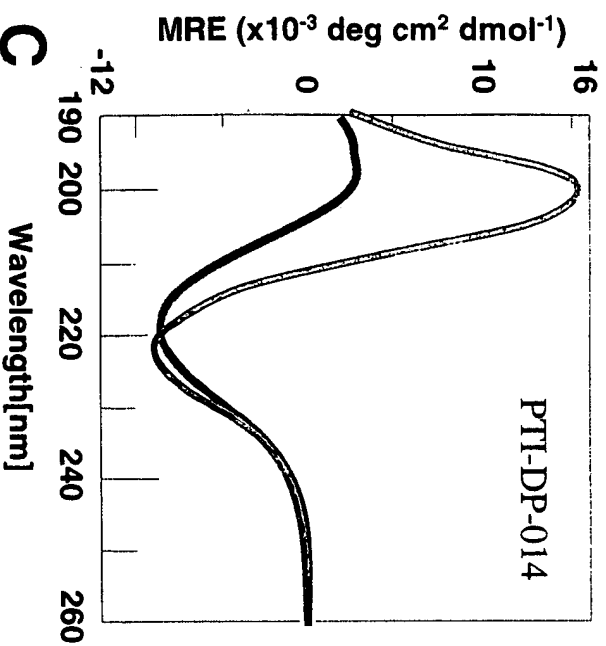
0.1 mg/ml —

PTI-compound only —

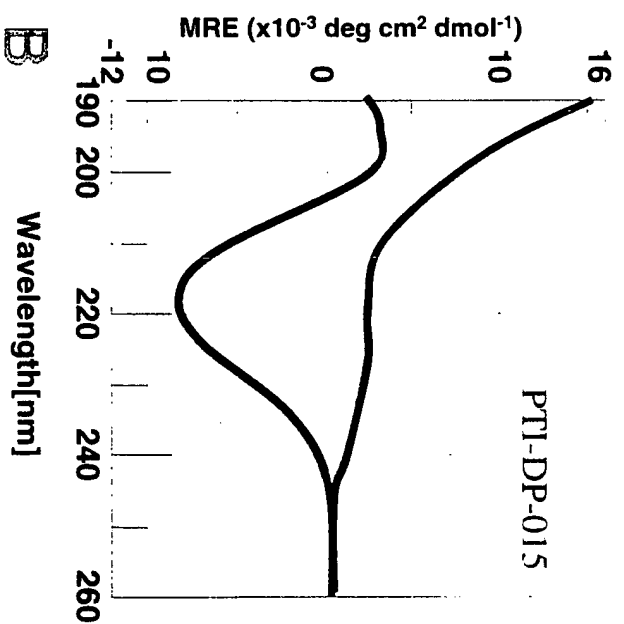
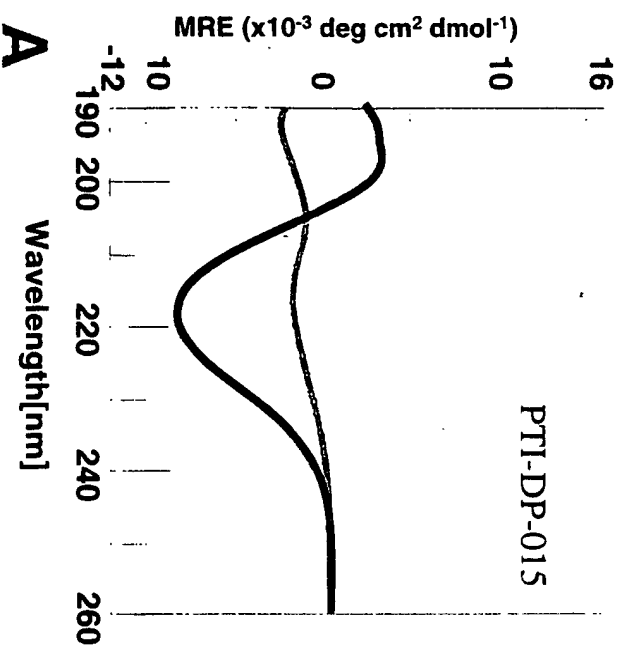
0.2 mg/ml —

Aβ42 + PTI-compound 1:2 w/wt —

Fig. 23



CD#33



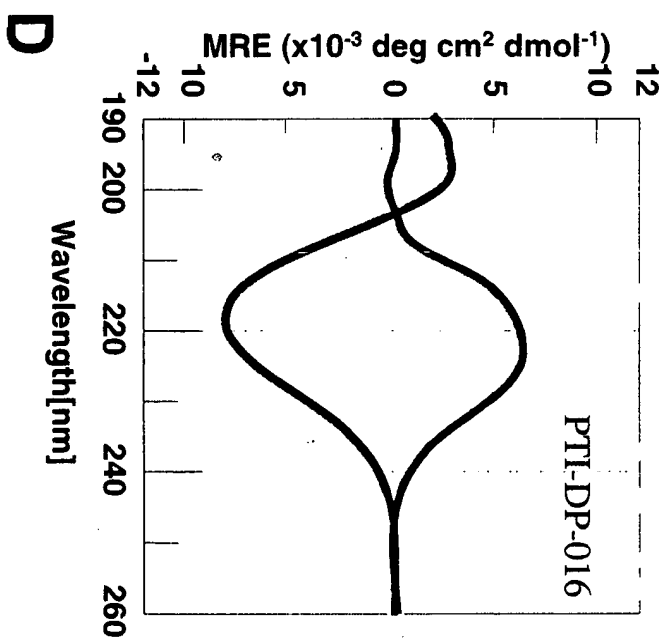
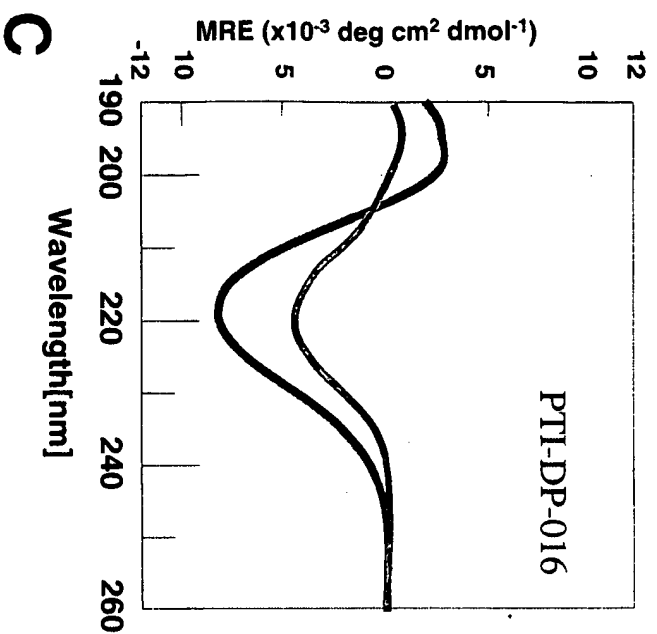
Legend:

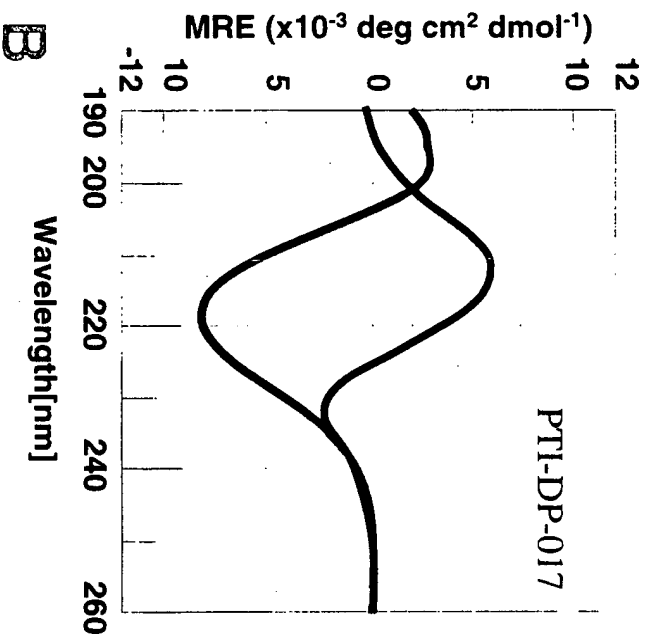
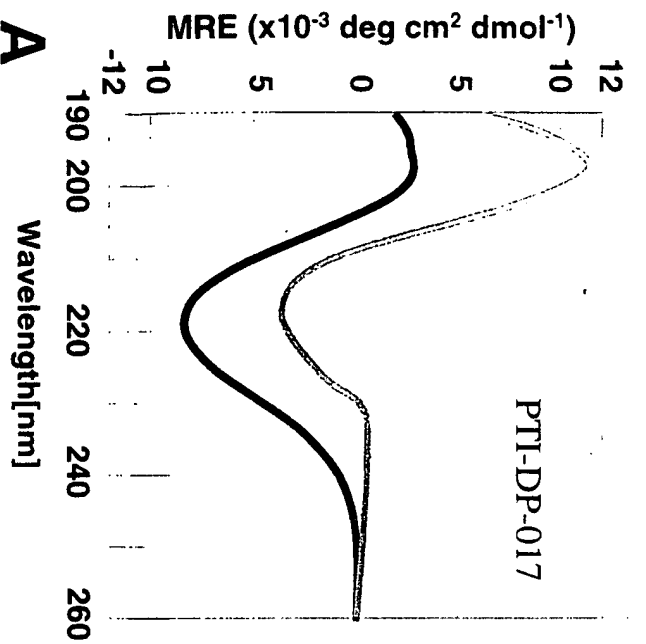
A β 42 Only —

PTI-compound only —

A β 42 + PTI-compound 1:2 w/wt —

Fig. 24





Legend:

Aβ42 Only —

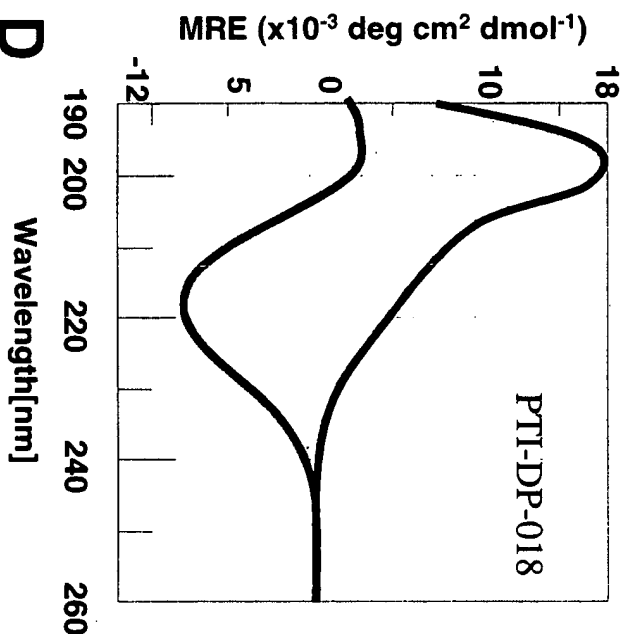
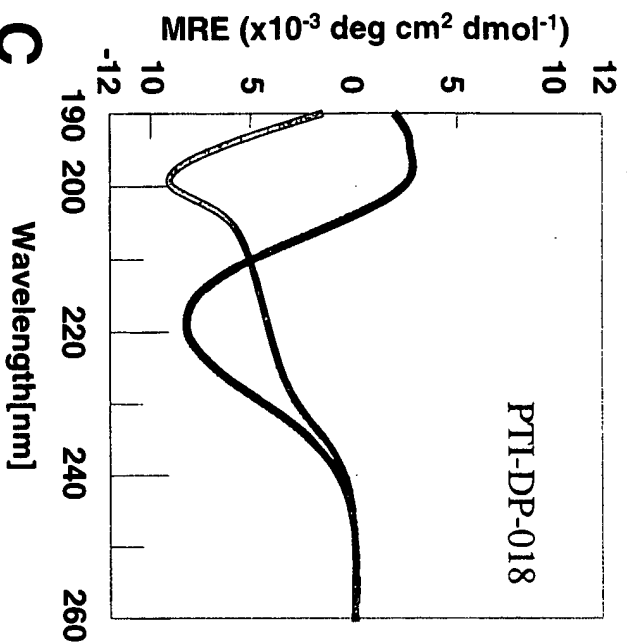
0.1 mg/ml —

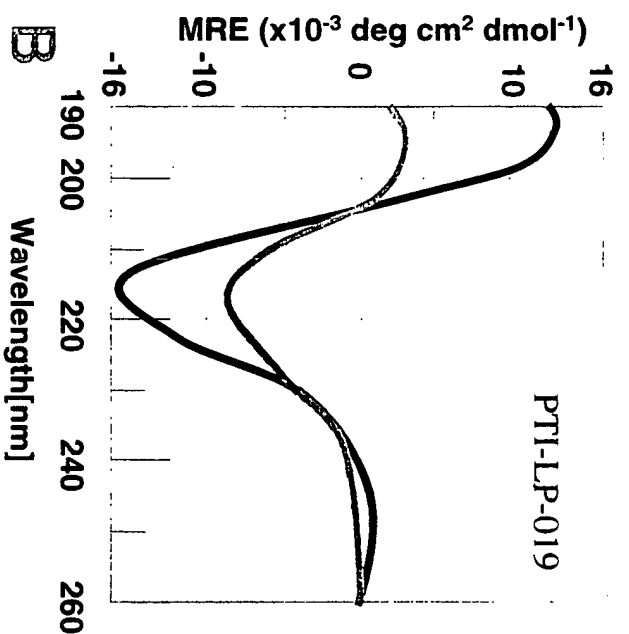
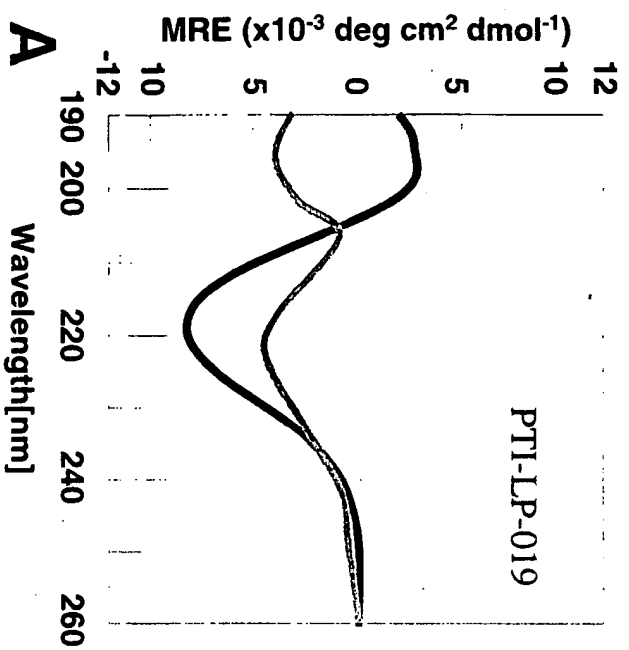
PTI-compound only —

0.2 mg/ml —

Aβ42 + PTI-compound 1:2 w/wl —

Fig. 25





Legend:

AB42 Only —

PTI-compound only —

AB42 + PTI-compound 1:2 wt/wt —

C

D